

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:20:49 ; Search time 76.2887 Seconds
(without alignments)
3001.261 Million cell updates/sec

Title: US-09-724-254A-3
Perfect score: 3124
Sequence: 1 MLWLWILLVLAPVSGQPART.....AEFSLTHFKNLFALSSFLP 592

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3111	99.6	592	4 AAB82314	Aab82314 Human imm
2	3111	99.6	592	7 ADM35236	Adm35236 Human LY1
3	2950	94.4	759	4 AAB82313	Aab82313 Human imm
4	2950	94.4	759	7 ADM35235	Adm35235 Human LY1
5	2950	94.4	977	4 AAB82315	Aab82315 Human imm
6	2950	94.4	977	6 ABP97215	Abp97215 Tumour-as
7	2950	94.4	977	7 ADM35237	Adm35237 Human LY1
8	2918.5	93.4	875	8 ABM82476	Abm82476 Human dia
9	2685.5	86.0	837	8 ABM82477	Abm82477 Human dia
10	1193.5	38.2	582	6 ABU99155	Abu99155 Novel hum
11	1193.5	38.2	582	8 ADM93875	Adm93875 Human NOV
12	1193.5	38.2	707	7 ADM06089	Adm06089 Human pro
13	1193.5	38.2	734	4 AAB82316	Aab82316 Human imm
14	1193.5	38.2	734	7 ADM35238	Adm35238 Human LY1
15	1193.5	38.2	750	8 ABM84916	Abm84916 Human dia
16	1191	38.1	733	8 ADL06557	Adl06557 Human tum
17	1176	37.6	727	6 ABB84668	Abb84668 Human SEC
18	1150.5	36.8	554	7 ADF74336	Adf74336 Extracell
19	1150.5	36.8	717	7 ADF74337	Adf74337 Human FcR
20	1150.5	36.8	717	7 ADF74318	Adf74318 Human FcR
21	1120	35.9	222	5 ABP69283	Abp69283 Human pol
22	1063.5	34.0	718	8 ABM84917	Abm84917 Human dia
23	1031	33.0	707	8 ABM84918	Abm84918 Human dia
24	952.5	30.5	641	8 ABM84919	Abm84919 Human dia
25	900	28.8	181	5 ABP51264	Abp51264 Human MDD

26	900	28.8	181	5 ABP51409	Abp51409 Human MDD
27	889.5	28.5	570	7 ADF74389	Adf74389 Murine Fc
28	889	28.5	468	7 ADF74391	Adf74391 Extracell
29	847.5	27.1	639	7 ADJ70604	Adj70604 Human hea
30	847.5	27.1	655	8 ABM84920	Abm84920 Human dia
31	826.5	26.5	515	4 AAB82312	Aab82312 Human imm
32	826.5	26.5	515	5 ABB80608	Abb80608 Human abg
33	826.5	26.5	515	7 ADM35234	Adm35234 Human LY1
34	826.5	26.5	515	8 ADP18669	Adp18669 Human pro
35	826	26.4	167	6 ABP75420	Abp75420 Human sec
36	803.5	25.7	421	6 ABU99156	Abu99156 Novel hum
37	803.5	25.7	421	6 ABU99157	Abu99157 Novel hum
38	803.5	25.7	421	8 ADM93877	Adm93877 Human NOV
39	786.5	25.2	421	6 ABU99158	Abu99158 Novel hum
40	786.5	25.2	421	8 ADM93881	Adm93881 Human NOV
41	783.5	25.1	445	7 ADM35268	Adm35268 Human LY1
42	773.5	24.8	508	4 AAB82317	Aab82317 Human imm
43	773.5	24.8	508	7 ADM35239	Adm35239 Human LY1
44	773.5	24.8	508	7 ADM35264	Adm35264 Human LY1
45	773.5	24.8	508	8 ADP89715	Adp89715 Human can

ALIGNMENTS

RESULT 1
AAB82314
ID AAB82314 standard; protein; 592 AA.

AC AAB82314;

XX 23-JUL-2001 (first entry)

DE Human immunoglobulin receptor isoform IRTA2b.

XX Immunoglobulin superfamily receptor translocation associated; IRTA;

KW IRTA2b; human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma;
KW myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..15

FT Protein /label= Signal_peptide

FT /label= Mature_protein

FT Modified-site 132..134

FT Modified-site /note= "Aen is N-glycosylated"

FT /note= "Aen is N-glycosylated"

FT /note= "Aen is N-glycosylated"

FT /note= "Aen is N-glycosylated"

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FT /note= "Aen is N-glycosylated"

FT /note= "Aen is N-glycosylated"

CC immunoglobulin superfamily receptor translocation associated protein
CC isoform 2b (IRTA2b), an FC receptor involved in the pathogenesis of
CC lymphoma and melanoma. Efforts to identify genes involved in chromosomal
CC aberrations affecting band 1q21 in multiple myeloma and B cell lymphoma
CC led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding
CC members of a novel subfamily of related receptors within the
CC immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA
CC isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82314 and AAB82315).
CC IRTA2b is a 592 amino acid glycoprotein, which diverges from IRTA2a at
CC residue 560, extending for a further 32 residues, whose hydrophobicity
CC suggest docking to the plasma membrane via a GPI anchor. The IRTA2 genes
CC display a specific pattern of expression in mature B cells. IRTA2 is
CC expressed in GC centrocytes and in perifollicular cells, which may
CC include immunoblasts and memory cells. The invention provides IRTA
CC nucleic acids and proteins, and antibodies directed to an epitope of an
CC IRTA protein. Methods are claimed for: detecting a B cell malignancy
CC comprising a 1q21 chromosomal rearrangement using a nucleic acid molecule
CC that specifically hybridises with a unique sequence of human IRTA1-5; and
CC treating a subject having a B cell cancer by administering an anti-IRTA
CC antibody or an antisense oligonucleotide that specifically hybridises to
CC IRTA mRNA so as to prevent overexpression of IRTA protein and hence to
CC arrest cell growth or induce cell death of cancer cells expressing IRTA.
CC The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma,
CC multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse
CC large cell lymphoma and follicular lymphoma. The B cell lymphoma is
CC selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-
CC Hodgkin's lymphoma
XX
SQ Sequence 592 AA;
Query Match 99.6%; Score 3111; DB 4; Length 592;
Best Local Similarity 99.7%; Pred. No. 3.8e-219; Indels 0; Gaps 0;
Matches 590; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPTVTFQGERVLTCKGFRFYSQKTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPTVTFQGERVLTCKGFRFYSQKTKWYHR 60
QY 61 YLKGKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDPSASLILOAPLSVFEQDSV 120
DB 61 YLKGKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDPSASLILOAPLSVFEQDSV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHPIHACLDKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHPIHACLDKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSFOPIGPNVTLCTQSLERSDVLPRFRDDQTLGLGWS 240
DB 181 VKIQVQEPFTRPVLRASSFOPIGPNVTLCTQSLERSDVLPRFRDDQTLGLGWS 240
QY 241 LSPNFQITAMWSKDSGFYWCCKAATPHSVISDSRSMIOQIIPASHPVLTLSPKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYWCCKAATPHSVISDSRSMIOQIIPASHPVLTLSPKALNFE 300
QY 301 GTKVTLHCETQEDSLRTLYRYHGVPLRHKSVCRCERGASISFSLTTENGNYCYTADNG 360
DB 301 GTKVTLHCETQEDSLRTLYRYHGVPLRHKSVCRCERGASISFSLTTENGNYCYTADNG 360
QY 361 LGAKPSKAVSLSVTPVPSHPVLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA 420
DB 361 LGAKPSKAVSLSVTPVPSHPVLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA 420
QY 421 LERRANSAGGVAISFSLTAHSGNYCYTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
DB 421 LERRANSAGGVAISFSLTAHSGNYCYTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
QY 481 EALTTEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPVGVRVSFSLTEGHSNYY 540
DB 481 EALTTEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPVGVRVSFSLTEGHSNYY 540
QY 541 CTADNGFGPQRSEVSLFVTGKCVLASKPPLAEFSLTHSKNLFALSSFLP 592
DB 541 CTADNGFGPQRSEVSLFVTGKCVLASHPPPLAEFSLTHSKNLFALSSFLP 592

RESULT 2
ADM35236
ID ADM35236 standard; protein; 592 AA.
XX
AC ADM35236;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human LXI48P cancer related protein for cancer detection method.
XX
KW cytotaxtic; T-cell vaccine; detection; cancer;
KW chronic lymphocytic leukemia.
XX
OS Homo sapiens.
XX
PN WO2003077836-A2.
XX
PD 25-SEP-2003.
XX
PF 06-NOV-2002; 2002WO-US035728.
XX
PR 06-NOV-2001; 2001US-00040862.
XX
PR 23-MAY-2002; 2002US-00154884.
XX
PA (CORI-) CORIXA CORP.
XX
PI Gaiger A, Algate PA, Mannion J, Retter M;
XX
DR WPI; 2003-756941/71.
XX
PT Detecting cancer in a patient comprises contacting a biological sample
PT from the patient with a binding agent that binds to a cancer-associated
PT polypeptide and comparing the amount of polypeptide to a predetermined
PT cutoff value.
XX
PS Disclosure; SEQ ID NO 10461; 419pp; English.
XX
CC The invention relates to a method of detecting (M1) cancer in a patient
CC by: (i) contacting a biological sample from the patient with an agent
CC that binds to any of three polypeptides given in the specification; (ii)
CC detecting in a sample an amount of the peptide that binds to the binding
CC agent; and (iii) comparing the amount of polypeptide present in the
CC patient's sample to a predetermined cutoff value. The specification also
CC discloses a separate method for detecting (M2) cancer in a patient by a
CC method similar to M1, except that the detection agent is an
CC oligonucleotide that binds to any of three polynucleotides given in the
CC specification. M1 and M2 are useful for detecting the presence of cancer
CC in a patient, especially chronic lymphocytic leukemia. The applicants
CC have identified specific human polypeptides overexpressed in one or more
CC types of hematological malignancies. This sequence corresponds to a
CC protein used in the method of the invention.
XX
SQ Sequence 592 AA;
Query Match 99.6%; Score 3111; DB 7; Length 592;
Best Local Similarity 99.7%; Pred. No. 3.8e-219; Indels 0; Gaps 0;
Matches 590; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPTVTFQGERVLTCKGFRFYSQKTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPTVTFQGERVLTCKGFRFYSQKTKWYHR 60
QY 61 YLKGKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDPSASLILOAPLSVFEQDSV 120
DB 61 YLKGKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDPSASLILOAPLSVFEQDSV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHPIHACLDKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHPIHACLDKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSFOPIGPNVTLCTQSLERSDVLPRFRDDQTLGLGWS 240

Db 181 VKIQVQEPFTRPVLRASSFQIPISGNPVTLTCTETSLERSDVPURFFRDDQTLGLGWS 240
Qy 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVISDSRPSWIQVQIPASHPVLTLSPKALNFE 300
Db 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVISDSRPSWIQVQIPASHPVLTLSPKALNFE 300
Qy 301 GTKVTLHCETQEDSLRTLRYFYHGVPLRHKSVCRCERGASISFSLTTENGNYCTADNG 360
Db 301 GTKVTLHCETQEDSLRTLRYFYHGVPLRHKSVCRCERGASISFSLTTENGNYCTADNG 360
Qy 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYOFHHEDAA 420
Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYOFHHEDAA 420
Qy 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSA 480
Db 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSA 480
Qy 481 EALTFFEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSPFSLTGHSGNYY 540
Db 481 EALTFFEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSPFSLTGHSGNYY 540
Qy 541 CTADNGFGPORSVSVSLFVTGKCWLASKPLAEFSLTHSFKNLFASSFLP 592
Db 541 CTADNGFGPORSVSVSLFVTGKCWLASHPPPLAEFSLTHSFKNLFASSFLP 592

RESULT 3
ID AAB82313 standard; protein; 759 AA.
XX AAB82313;
AC AAB82313;
XX AAB82313;
DT 23-JUL-2001 (first entry)
XX Human immunoglobulin receptor isoform IRTA2a.
DE Human immunoglobulin receptor translocation associated; IRTA;
KW IRTA2a; human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma;
KW myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.
XX Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..15
FT /label= signal_peptide
FT Protein 16..759
FT /label= mature_protein
FT Modified-site 132..134
FT /note= "Asn is N-glycosylated"
FT Modified-site 383..385
FT /note= "Asn is N-glycosylated"
FT Modified-site 621..623
FT /note= "Asn is N-glycosylated"
FT Modified-site 631..633
FT /note= "Asn is N-glycosylated"
FT Modified-site 714..716
FT /note= "Asn is N-glycosylated"
XX W0200138490-A2.
PN 31-MAY-2001.
XX 28-NOV-2000; 2000WO-US032403.
XX 29-NOV-1999; 99US-0168151P.
XX (UYCO) UNIV COLUMBIA NEW YORK.
PA Dalla-Favera R;
XX WPI; 2001-355921/37.

DR N-PSDB; AAF30950.
XX New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor
PT Translocation Associated proteins, used to treat B cell malignancies
PT including lymphomas and multiple myeloma.
XX Claim 3; Fig 18B-1-18B-2; 72pp; English.
XX The present sequence is that of the novel human immunoglobulin receptor,
CC immunoglobulin superfamily receptor translocation associated protein
CC isoform 2a (IRTA2a), an Fc receptor involved in the pathogenesis of
CC lymphoma and melanoma. Efforts to identify genes involved in chromosomal
CC aberrations affecting band 1q21 in multiple myeloma and B cell lymphoma
CC led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding
CC members of a novel subfamily of related receptors within the
CC immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA
CC isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82314 and AAB82315).
CC IRTA2a is a 759 amino acid secreted glycoprotein with 8 Ig-type domains
CC followed by a unique C-terminus. IRTA2b diverges from IRTA2a at residue
CC 560, extending for a further 32 residues. IRTA2c diverges from IRTA2a at
CC residue 746 and extends for a further 231 residues. The IRTA genes
CC display a specific pattern of expression in mature B cells. IRTA2 is
CC expressed in GC centrocytes and in perfollicular cells, which may
CC include immunoblasts and memory cells. The invention provides IRTA
CC nucleic acids and proteins, and antibodies directed to an epitope of an
CC IRTA protein. Methods are claimed for: detecting a B cell malignancy
CC comprising a 1q21 chromosomal rearrangement using a nucleic acid molecule
CC that specifically hybridises with a unique sequence of human IRTA1-5; and
CC treating a subject having a B cell cancer by administering an anti-IRTA
CC antibody or an antisense oligonucleotide that specifically hybridises to
CC IRTA mRNA so as to prevent overexpression of IRTA protein and hence to
CC arrest cell growth or induce cell death of cancer cells expressing IRTA.
CC The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma,
CC multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse
CC large cell lymphoma and follicular lymphoma. The B cell lymphoma is
CC selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-
CC Hodgkin's lymphoma
XX Sequence 759 AA;
Qy Query Match 94.4%; Score 2950; DB 4; Length 759;
Db Best Local Similarity 98.4%; Pred. No. 3.3e-207;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;
Qy 1 MLILVILLVLPVSGQFARTPRPIIFLOPPVTTVFOGERVTLTKGFRFSPQTKWYHR 60
Db 1 MLILVILLVLPVSGQFARTPRPIIFLOPPVTTVFOGERVTLTKGFRFSPQTKWYHR 60
Qy 61 YLGKEILRETDPNILEVQSGEYRCQAQGSPLSSPVHLPSSASLILQAPLSVFEQDSVV 120
Db 61 YLGKEILRETDPNILEVQSGEYRCQAQGSPLSSPVHLPSSASLILQAPLSVFEQDSVV 120
Qy 121 LRCRAKAEVTLANTTIYKNDNLVLAFLNKRTRDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLANTTIYKNDNLVLAFLNKRTRDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180
Qy 181 VKIQVQEPFTRPVLRASSFQIPISGNPVTLTCTETSLERSDVPURFFRDDQTLGLGWS 240
Db 181 VKIQVQEPFTRPVLRASSFQIPISGNPVTLTCTETSLERSDVPURFFRDDQTLGLGWS 240
Qy 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVISDSRPSWIQVQIPASHPVLTLSPKALNFE 300
Db 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVISDSRPSWIQVQIPASHPVLTLSPKALNFE 300
Qy 301 GTKVTLHCETQEDSLRTLRYFYHGVPLRHKSVCRCERGASISFSLTTENGNYCTADNG 360
Db 301 GTKVTLHCETQEDSLRTLRYFYHGVPLRHKSVCRCERGASISFSLTTENGNYCTADNG 360
Qy 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYOFHHEDAA 420
Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYOFHHEDAA 420
Qy 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSA 480

Db 421 LERRSAGGVAISFSLTAHSGNYICTADNGFQQRKAVSLIIVPVSHPVLTLSA 480
QY 481 EALTPEGATVTLHCEVQSGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGY 540
Db 481 EALTPEGATVTLHCEVQSGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGY 540
QY 541 CTADNGFGQRSEVVSFLFTGKCVLASKPPL 572
Db 541 CTADNGFGQRSEVVSFLFTGKCVLASKPPL 568
RESULT 4
ADM35235
ID ADM35235 standard; protein; 759 AA.
XX AC ADM35235;
XX DT 03-JUN-2004 (first entry)
XX Human LX148P cancer related protein for cancer detection method.
XX cytostatic; T-cell vaccine; detection; cancer;
XX chronic lymphocytic leukemia.
XX Homo sapiens.
XX WO2003077836-A2.
XX 25-SEP-2003.
XX 06-NOV-2002; 2002WO-US035728.
XX 06-NOV-2001; 2001US-00040862.
XX 23-MAY-2002; 2002US-00154884.
XX (CORI-) CORIXA CORP.
XX Gaiger A, Algate PA, Mannion J, Retter M;
XX WPI; 2003-756941/71.
XX Detecting cancer in a patient comprises contacting a biological sample
XX from the patient with a binding agent that binds to a cancer-associated
XX polypeptide and comparing the amount of polypeptide to a predetermined
XX cutoff value.
XX Disclosure; SEQ ID NO 10460; 419pp; English.
XX The invention relates to a method of detecting (M1) cancer in a patient
XX by: (i) contacting a biological sample from the patient with an agent
XX that binds to any of three polypeptides given in the specification; (ii)
XX detecting in a sample an amount of the peptide that binds to the binding
XX agent; and (iii) comparing the amount of polypeptide present in the
XX patient's sample to a predetermined cutoff value. The specification also
XX discloses a separate method for detecting (M2) cancer in a patient by a
XX method similar to M1, except that the detection agent is an
XX oligonucleotide that binds to any of three polynucleotides given in the
XX specification. M1 and M2 are useful for detecting the presence of cancer
XX in a patient, especially chronic lymphocytic leukemia. The applicants
XX have identified specific human polypeptides overexpressed in one or more
XX types of hematological malignancies. This sequence corresponds to a
XX protein used in the method of the invention.
XX
XX Sequence 759 AA;
Query Match 94.4%; Score 2950; DB 7; Length 759;
Best Local Similarity 98.4%; Pred. No. 3.3e-207;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;
QY 1 MLLWVILLVAPVSGGFARTPRILFLQPPWTTVFGERVTLTCGFRFYSQKTKWYHR 60
Db 1 MLLWVILLVAPVSGGFARTPRILFLQPPWTTVFGERVTLTCGFRFYSQKTKWYHR 60

QY 61 YLGKILRETPDNIILEVOESGEYRCOAGSPSSPVHLDFFSSASLILQAPLSVFEGDSV 120
Db 61 YLGKILRETPDNIILEVOESGEYRCOAGSPSSPVHLDFFSSASLILQAPLSVFEGDSV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFHACIKDNGAYRGTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFHACIKDNGAYRGTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSPQISGNPVTITCTQSLERSDVLPRFRFRDDQTILGLWS 240
Db 181 VKIQVQEPFTRPVLRASSPQISGNPVTITCTQSLERSDVLPRFRFRDDQTILGLWS 240
QY 241 LSPNFOITAMWSKDSGFYWCATMPHVSIVSDSPRSWIOVQIPASHPVLTLSPEKALNPE 300
Db 241 LSPNFOITAMWSKDSGFYWCATMPHVSIVSDSPRSWIOVQIPASHPVLTLSPEKALNPE 300
QY 301 GTKVTLHCETOEDSLRTLYRFYHGVPLRHKSVRCERGASISFSLTTENSGNYICTADNG 360
Db 301 GTKVTLHCETOEDSLRTLYRFYHGVPLRHKSVRCERGASISFSLTTENSGNYICTADNG 360
QY 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDILIFGAKVTLHCEAQRGSLPILYQFHEDAA 420
Db 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDILIFGAKVTLHCEAQRGSLPILYQFHEDAA 420
QY 421 LERRSANSAGVAISFSLTAHSGNYICTADNGFGQRKAVSLIIVPVSHPVLTLSA 480
Db 421 LERRSANSAGVAISFSLTAHSGNYICTADNGFGQRKAVSLIIVPVSHPVLTLSA 480
QY 481 EALTPEGATVTLHCEVQSGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGY 540
Db 481 EALTPEGATVTLHCEVQSGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGY 540
QY 541 CTADNGFGQRSEVVSFLFTGKCVLASKPPL 572
Db 541 CTADNGFGQRSEVVSFLFTGKCVLASKPPL 568
RESULT 5
AAB82315
ID AAB82315 standard; protein; 977 AA.
XX AC AAB82315;
XX DT 23-JUL-2001 (first entry)
XX Human immunoglobulin receptor isoform IRTA2c.
XX Immunoglobulin superfamily receptor translocation associated; IRTA;
XX IRTA2c; human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma;
XX myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.
XX Homo sapiens.
Key Location/Qualifiers
Peptide 1..15
Protein /label= Signal_peptide
Modified-site /label= Mature_protein
Modified-site 132..134 /note= "Asn is N-glycosylated"
Modified-site 383..385 /note= "Asn is N-glycosylated"
Modified-site 621..623 /note= "Asn is N-glycosylated"
Modified-site 631..633 /note= "Asn is N-glycosylated"
Modified-site 714..716 /note= "Asn is N-glycosylated"
Modified-site 795..797 /note= "Asn is N-glycosylated"
Modified-site 806..808 /note= "Asn is N-glycosylated"

FT	Modified-site	816..818 /note= "Asn is N-glycosylated"
FT	Modified-site	843..845 /note= "Asn is N-glycosylated"
FT	Domain	851..873 /note= "transmembrane domain"
FT	Binding-site	899..902 /note= "putative consensus Src-homology 2 (SH2) binding domain"
FT	Binding-site	924..927 /note= "putative consensus Src-homology 2 (SH2) binding domain"
FT	Binding-site	954..957 /note= "putative consensus Src-homology 2 (SH2) binding domain"
XX		WO200138490-A2.
PX		31-MAY-2001.
PP		28-NOV-2000; 2000WO-US032403.
XX		29-NOV-1999; 99US-0168151P.
PR		(UYCO) UNIV COLUMBIA NEW YORK.
PA		Dalla-Favera R;
XX		WPI: 2001-355921/37.
DR		N-PSDB; AAF30952.
XX		New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor Translocation Associated proteins, used to treat B cell malignancies including lymphomas and multiple myeloma.
PS		Claim 3; Fig 18B-1-18B-2; 72pp; English.
XX		The present sequence is that of the novel human immunoglobulin receptor, immunoglobulin superfamily receptor translocation associated protein isoform 2c (IRTA2c), an Fc receptor involved in the pathogenesis of lymphoma and melanoma. Efforts to identify genes involved in chromosomal aberrations affecting band Ig21 in multiple myeloma and B cell lymphoma led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding members of a novel subfamily of related receptors within the immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82313 and AAB82314). IRTA2c is the longest isoform. It is a type I transmembrane glycoprotein. Each SH2 binding site agrees with the immune receptor tyrosine-based inhibition motif (ITIM) consensus and is encoded by a separate exon. The IRTA genes display a specific pattern of expression in mature B cells. IRTA2 is expressed in GC centrocytes and in perifollicular cells, which may include immunoblasts and memory cells. The invention provides IRTA nucleic acids and proteins, and antibodies directed to epitopes of IRTA proteins. Methods are claimed for: detecting a B cell malignancy comprising a Ig21 chromosomal rearrangement using a nucleic acid molecule that specifically hybridises with a unique sequence of human IRTA1-5; and treating a subject having a B cell cancer by administering an anti-IRTA antibody or an antisense oligonucleotide that specifically hybridises to IRTA mRNA so as to prevent overexpression of IRTA protein and hence to arrest cell growth or induce cell death of cancer cells expressing IRTA. The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma, multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse large cell lymphoma and follicular lymphoma. The B cell lymphoma is selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-Hodgkin's lymphoma
XX		Sequence 977 AA;
SQ		Query Match 94.4%; Score 2950; DB 4; Length 977; Best Local Similarity 98.4%; Pred. No. 4.7e-207; Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;
QY		1 MLLWLVLAPVSGQFARTPRPIIFLOPPWTTFVQGERVLTCTCKGFRFYSPQKTKMYHR 60

Qy 1 MLLWVILLVAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQTKWYHR 60

XX	WPI; 2003-354551/33.
DR	N-PSDB; ACC49533.
XX	New antibodies against tumor-associated antigenic target polypeptide,
PT	useful for treating or diagnosing tumors or cancers in mammals; e.g.,
PT	prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
PT	carcinomas.
XX	
PS	Claim 2; Fig 97; 285pp; English.
XX	
CC	ACC49493 to ACC49552 encode the human tumour-associated antigenic target
CC	(TAT) proteins given in ABP371175 to ABP97234. The present invention
CC	describes an isolated antibody that binds to a polypeptide having at
CC	least 80 % sequence identity to any of the 60 150-800 residue amino acid
CC	sequences (S1), given in ABP97175 to ABP97234, comprising (S1), lacking
CC	its associated signal peptide, encoded by any of the 60 2000-3000 base
CC	pair sequences (S2), given in ACC49493 to ACC49552. TAT proteins have
CC	cytostatic activity. The antibody can be used for treating or diagnosing
CC	tumours or cancers in mammals, e.g. prostate cancer, lung cancer, breast
CC	cancer, colon cancer, ovarian cancer, prostate adenocarcinomas, renal
CC	cell carcinomas, or thyroid cancer
XX	
SQ	Sequence 977 AA;
	Query Match 94.4%; Score 2950; DB 6; Length 977;
	Best Local Similarity 98.4%; Pred. No. 4.7e-207;
	Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;
OY	1 MLLWVILLVLAPVSGQFARTPRPIIFLQPWTTFQGERVTLCCKGFRFYSPQKTKWYHR 60
Db	1 MLLWVILLVLAPVSGQFARTPRPIIFLQPWTTFQGERVTLCCKGFRFYSPQKTKWYHR 60
OY	61 YLGKEILRETNDNILEVOESGEYRCAQGSPFLDFSSASLILOAPLSVFEGDSVV 120
Db	61 YLGKEILRETNDNILEVOESGEYRCAQGPLSLFPVHLDFFSSASLILOAPLSVFEGDSVV 120
OY	121 LRCRAKAVETLNNTIYKNDNVLAFLNKRTDPhiPHACLKONGAYRCTGYKESCPCVSST 180
Db	121 LRCRAKAVETLNNTIYKNDNVLAFLNKRTDPhiPHACLKONGAYRCTGYKESCPCVSST 180
OY	181 VKIQVEPPTRPVLRASSFQIPISGNPNVLTCTETOLSLERSDVPLRFRFRDDQTGLGWS 240
Db	181 VKIQVEPPTRPVLRASSFQIPISGNPNVLTCTETOLSLERSDVPLRFRFRDDQTGLGWS 240
OY	241 LSNFOITAMWKSDGSFYWCKAATMHPHSVISDSPRSMTQVQIPASHPVLTLSPEKALNFE 300
Db	241 LSNFOITAMWKSDGSFYWCKAATMHPHSVISDSPRSMTQVQIPASHPVLTLSPEKALNFE 300
OY	301 GTKVTLHCETQDSLRTLRYFYHEGVPLRHKSVCERCASISFSLTTSNSNYICTADNG 360
Db	301 GTKVTLHCETQDSLRTLRYFYHEGVPLRHKSVCERCASISFSLTTSNSNYICTADNG 360
OY	361 LGAKPKSAVLSVTVPVSHPVNLNSPEDLIEFGAKVTLHCEAQRGSLPILYQFHEDAA 420
Db	361 LGAKPKSAVLSVTVPVSHPVNLNSPEDLIEFGAKVTLHCEAQRGSLPILYQFHEDAA 420
OY	421 LERRSANSAGGVAISFSLTAHSGNYICTADNGFGQSRKAVLSLITVPVSHPVLTLSA 480
Db	421 LERRSANSAGGVAISFSLTAHSGNYICTADNGFGQSRKAVLSLITVPVSHPVLTLSA 480
OY	481 EALTFFGATVTLHCEVQRGSPQILYOFYHEDMPLVSSSTPSVGRVSFSPSLTEGHSGNY 540
Db	481 EALTFFGATVTLHCEVQRGSPQILYOFYHEDMPLVSSSTPSVGRVSFSPSLTEGHSGNY 540
OY	541 CTADNGFGPORSEVSVLFVTGKCWLASKPPL 572
Db	541 CTADNGFGPORSEVSVLFVT---VPVSRPIL 568
	RESULT 7
	ADM35237
	TID ADM15237 standard; protein; 977 AA.

Db 241 LSPNQITAMWSKDSGFYCKAATMPHSHVSDSPRSWIQVOIPASHVPLTSLSPKALNFE 300
Qy 301 GTKVTLCETQEDSLRTLYRFYHEGVPLRHKSVCRCGASISFSLTTTNSGNYCTADNG 360
Db 301 GTKVTLCETQEDSLRTLYRFYHEGVPLRHKSVCRCGASISFSLTTTNSGNYCTADNG 360
Qy 361 LGAKPSKAVSLSVTPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA 420
Db 361 LGAKPSKAVSLSVTPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA 420
Qy 421 LERRSANSAGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSVTPVSHVPLTSLSSA 480
Db 421 LERRSANSAGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSVTPVSHVPLTSLSSA 480
Qy 481 EALTFFEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGYY 540
Db 481 EALTFFEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGYY 540
Qy 541 CTADNGFGPORSSEVSLFVTGKCWLASKPPL 572
Db 541 CTADNGFGPORSSEVSLFVTGKCWLASKPPL 568

RESULT 8
ABM82476
ID ABM82476 standard; protein; 875 AA.
AC ABM82476;
XX
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2725.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
XX 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
XX (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthehorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Paralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtzen ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
XX WPI: 2004-329368/30.
DR N-PSDB; ACN41128.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,

CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 875 AA;
Query Match 93.4%; Score 2918.5; DB 8; Length 875;
Best Local Similarity 97.4%; Pred. No. 8.2e-205;
Matches 557; Conservative 3; Mismatches 9; Indels 3; Gaps 1;
Qy 1 MLLWVILLVLPVSGQPARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSPOKTKWYHR 60
Db 1 MLLWVILLVLPVSGQPARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSPOKTKWYHR 60
Qy 61 YLGKEILRETPDNILEVOESGEYRCQAQSPVHLDFSSASLILOAPLSVEGDSVV 120
Db 61 YLGKEILRETPDNILEVOESGEYRCQAQSPVHLDFSSASLILOAPLSVEGDSVV 120
Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHACLDKNGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHACLDKNGAYRCTGYKESCCPVSSNT 180
Qy 181 VKIQVQEPFTRPVLRASSFQPIISGNPVTLTCETQLSLERSDVPLRFRDDQTLGLWS 240
Db 181 VKIQVQEPFTRPVLRASSFQPIISGNPVTLTCETQLSLERSDVPLRFRDDQTLGLWS 240
Qy 241 LSPNFOITAMWSKDSGFYCKAATMPHSHVSDSPRSWIQVOIPASHVPLTSLSPKALNFE 300
Db 241 LSPNFOITAMWSKDSGFYCKAATMPHSHVSDSPRSWIQVOIPASHVPLTSLSPKALNFE 300
Qy 301 GTKVTLCETQEDSLRTLYRFYHEGVPLRHKSVCRCGASISFSLTTTNSGNYCTADNG 360
Db 301 GTKVTLCETQEDSLRTLYRFYHEGVPLRHKSVCRCGASISFSLTTTNSGNYCTADNG 360
Qy 361 LGAKPSKAVSLSVTPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA 420
Db 361 LGAKPSKAVSLSVTPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA 420
Qy 421 LERRSANSAGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSVTPVSHVPLTSLSSA 480
Db 421 LERRSANSAGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSVTPVSHVPLTSLSSA 480
Qy 481 EALTFFEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGYY 540
Db 481 EALTFFEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGYY 540
Qy 541 CTADNGFGPORSSEVSLFVTGKCWLASKPPL 572
Db 541 CTADNGFGPORSSEVSLFVTGKCWLASKPPL 569

RESULT 9
ABM82477
ID ABM82477 standard; protein; 837 AA.
XX
XX AC ABM82477;
XX
XX DT 18-NOV-2004 (first entry)
XX
XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:2726.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
XX PN WO2004023973-A2.

XX PD 25-MAR-2004.
XX PF 12-SEP-2003; 2003WO-US028227.
XX PR 12-SEP-2002; 2002US-0410259P.
XX PR 12-SEP-2002; 2002US-0410260P.
XX PA (INCY-) INCYTE CORP.
XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Deleagane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez Cu;
XX WPI; 2004-329368/30.
DR N-PSDB; ACN41129.
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX Claim 27; Page; 190pp; English.
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX SQ Sequence 837 AA;
Query Match 86.08; Score 2685.5; DB 8; Length 837;
Best Local Similarity 90.64; Pred. No. 9.1e-188;
Matches 518; Conservative 3; Mismatches 10; Indels 41; Gaps 2;
QY 1 MLLWVILLVAPVSGQPARTPRPIIFLQPPWTVFQGERVTLTKGFRFYSPOKTKWYHR 60
DB 1 MLLWVILLVAPVSGQPARTPRPIIFLQPPWTVFQGERVTLTKGFRFYSPOKTKWYHR 60
QY 61 YLGEKILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFFSSASLLIQAELSVEGDSVV 120
DB 61 YLGEKILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFFSSASLLIQAELSVEGDSVV 120
QY 121 LRCRAKAEVLNNTIYKNDVNLAFLNKRTDFPHACLKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVLNNTIYKNDVNLAFLNKRTDFPHACLKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSFOIPISGNPVTLCETQLSLERSDVLPRFFRDQDTGLGWS 240
DB 181 VKIQVQEPFTRPVLRASSFOIPISGNPVTLCETQLSLERSDVLPRFFRDQDTGLGWS 240
QY 241 LSPNFQITAMWKSQSGFVWCKAAATMPHSVLSDSRSMIQVQIPASHPVLTLSPKALNFE 300
DB 241 LSPNFQITAMWKSQSGFVWCKAAATMPHSVLSDSRSMIQVQIPASHPVLTLSPKALNFE 300
QY 301 GTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVRCERGASISFSLTTTENGNYCYCTADNG 360

DB 282 -----XFYHEGVPLRHKSVRCERGASISFSLTTTENGNYCYCTADNG 322
QY 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQPHHEDAA 420
DB 323 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQPHHEDAA 382
QY 421 LERSANSAGGVAISFSLTAHSGNYCYCTADNGFGPORSKAVSLSVTVPVSHPVLTLSA 480
DB 383 LERSANSAGGVAISFSLTAHSGNYCYCTADNGFGPORSKAVSLSVTVPVSHPVLTLSA 442
QY 481 EALTPEGATVTLHCEVQSGPQIILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY 540
DB 443 EALTPEGATVTLHCEVQSGPQIILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY 502
QY 541 CTADNGFGPORSSEVVSFLVTKCKWVLASKPPL 572
DB 503 CTADNGFGPORSSEVVSFSLS---VPVSRPIL 531
RESULT 10
ABU99155
ID ABU99155 standard; protein; 582 AA.
XX AC ABU99155;
XX DT 01-AUG-2003 (first entry)
XX DE Novel human GPCR related protein NOV17a.
XX KW Human; G-protein coupled receptor related protein; GPCR related protein;
KW NOV; cytostatic; cardiac; antiarteriosclerotic; antidiabetic;
KW immunomodulator; anti-HIV; anorectic; antiasthmatic; haemostatic;
KW antiparkinsonian; neuroprotective; nootropic; gene therapy; vaccine;
KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer;
KW diabetes; immune disorder; AIDS; obesity; asthma;
KW haematopoietic disorder; Parkinson's disease; Alzheimer's disease;
KW infection; multiple sclerosis; cancer-associated cachexia;
KW wasting disorder; chronic disease; neurogenesis; cell differentiation;
KW cell proliferation; haematopoiesis; wound healing; angiogenesis;
KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.
XX OS Homo sapiens.
XX PN WO200299116-A2.
XX PD 12-DEC-2002.
XX PF 04-JUN-2002; 2002WO-US017428.
XX PR 04-JUN-2001; 2001US-0295607P.
XX PR 04-JUN-2001; 2001US-0295661P.
XX PR 06-JUN-2001; 2001US-0296404P.
XX PR 06-JUN-2001; 2001US-0296418P.
XX PR 14-JUN-2001; 2001US-0298285P.
XX PR 15-JUN-2001; 2001US-0298556P.
XX PR 21-JUN-2001; 2001US-0299949P.
XX PR 26-JUN-2001; 2001US-0300883P.
XX PR 28-JUN-2001; 2001US-0301550P.
XX PR 13-AUG-2001; 2001US-0311972P.
XX PR 27-AUG-2001; 2001US-0315071P.
XX PR 29-AUG-2001; 2001US-0315660P.
XX PR 14-SEP-2001; 2001US-0322293P.
XX PR 17-SEP-2001; 2001US-0322706P.
XX PR 14-DEC-2001; 2001US-0341186P.
XX PR 28-FEB-2002; 2002US-0361189P.
XX PR 12-MAR-2002; 2002US-0363673P.
XX PR 03-JUN-2002; 2002US-0363676P.
XX (CURA-) CURAGEN CORP.
XX PA Anderson DW, Baumgartner JC, Boldog FL, Casman SJ, Edinger SR;
XX PI

PI Gangolli EA, Gerlach VL, Gorman L, Guo X, Hjal T, Kekuda R, Li L;
PI MacDougall JR, Malvankar UM, Millet I, Padigaru M, Patturajan M;
PI Pena CE, Rastelli L, Shimkets RA, Stone DU, Spytek KA, Vernet CM;
PI Voss EZ, Zerhusen BD;
XX WPI: 2003-140627/13.
DR N-PSDB; ACD03659.
XX
XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Claim 1; Page 166; 332pp; English.
XX
XX The invention describes an isolated polypeptide (I) comprising any of 27
CC 118-961 residue amino acid sequences, given in the specification, a
CC mature form of them, a sequence that is at least 95 % identical to them,
CC or a sequence having one or more conservative substitutions in them. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease selected from a pathology
CC associated with the polypeptide. The NOVX polypeptides, polynucleotides
CC and antibodies are useful in treating or preventing NOVX-associated
CC disorders, e.g. cardiomyopathy, atherosclerosis, cancer, diabetes, immune
CC disorders, AIDS, obesity, asthma, haematopoietic disorders, Parkinson's
CC disease, Alzheimer's disease, infections, multiple sclerosis, cancer-
CC associated cachexia, and other wasting disorders associated with chronic
CC diseases. The nucleic acids and polypeptides may also be used as targets
CC for the identification of small molecules that modulate or inhibit e.g.
CC neurogenesis, cell differentiation, cell proliferation, haematopoiesis,
CC wound healing and angiogenesis, in gene therapy, in generation of
CC antibodies that bind immunospecifically to NOVX substances for use in
CC therapeutic or diagnostic methods. The nucleic acids are further used as
CC hybridisation probes, in chromosome mapping, tissue typing, preventive
CC medicine, and pharmacogenomics. The polypeptides are also useful as
CC vaccines. This is the amino acid sequence of a novel human G-protein
CC coupled receptor related protein NOV
XX
SQ Sequence 582 AA;

Query Match 38.2%; Score 1193.5; DB 6; Length 582;
Best Local Similarity 45.5%; Pred. No. 1.2e-78;
Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;

QY 1 MLLWVILLVAPVSGQPARTPRPIIFLOPPWTVFGQERVLTCKGFRFYSPQ-KTKWYH 59
DB 1 MLLWLLLLIITPREGQGVAPKAVLLNPNPSTAFKGEKVALICSSISHSLAQDIYWH 60

QY 60 RYLGKEILRTPDNILEVQSGEYRCOAQSGPLSPVHLDFSSASLILOAPLSVFEGDSV 119
DB 61 ---DEKLLTKHKDKI-QITEFGNYQCKTRGSSLSDAVHVEFSPDWLILQALHPVFECDNV 116

QY 120 VLRCAKAEVTLNNTIYKNDVLAFLNKRDFHHPACLKNGAYRGTGYKESC---CPV 176
DB 117 ILRCQKQKNDKNTKQVYKDGKQKLPNSNLEKTIIVNSVRDNSKSYCHTAYRKFYILDIEV 176

QY 177 SSNTVKIQVEPTFRPVLRASSFPQISGNPVLTTCQLSLERSDPLRFRFRDDQTLG 236
DB 177 TSFPLNIQVELFHPVLRASSFTPEGSPMTLTCTQLSPQDPDVLQPSLFRDSQTLG 236

QY 237 LGWSLSPNFOITAMWSKDSGFYCKAATMPHSVISDSRSMIQV-IPASHPVLTLSPEK 295
DB 237 LGWSRSPRLQIPAMWTEDSGYVCEVETVTHSIKGRSLRQIRVQRPVPSNVNLEIRPTG 296

QY 296 ALNFEGTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVRCERGASISFSLTT---ENSGN 352
DB 297 GQIIEGNMVLICVSAQSGSTVTFSSWHKEG-RVRSLGKRTQRSLLAEHLVLTVKESDAGR 355

QY 353 YYCTADNGLGAKPSKAVSLSVTPVSHPVNLNLSPEDLIEPEGAKVTLHCQAQSGSPILY 412
DB 356 YYCAADNVHSPILSTWIRVTRVPVSHPVLTFRAPRAHTVVGDLLELHCESLGRSPILY 415

QY 413 QFHHEDAALERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSH 472

Db 416 RFYHEDVTLGNSAPSGGASFNLSLTAHSGNYSADADNGLGAQHSHGVSLRVTPVSR 475
QY 473 PVLTSSAALTEPEGATVTLHCEVQVQSGPOILYQFYHEDMPLVSSSTPSPVGRVYFSFSLT 532
Db 476 PVLTLPAGQAQVVGDLLELHCESLGRSPILYWFYHEDDTLGNISAHSGGASFNLSLT 535
QY 533 EGHSGNYCTADNGFGPQRSEVSVLFTVG 561
Db 536 TEHSGNYSCEADNGLGAQHSHKVTLNVTG 564

RESULT 11
ADM93875
ID ADM93875 standard; protein; 582 AA.
XX
AC ADM93875;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human NOV protein #47.
XX
KW gene therapy; vaccine; NOVX; cancer; neurodegenerative disorder;
KW Parkinson's disease; metabolic disorder; diabetes; obesity;
KW immune related disorder; tissue typing; human.
XX
OS Homo sapiens.
XX
PN US2004009480-A1.
XX
PD 15-JAN-2004.
XX
XX 03-JUN-2002; 2002US-00162335.
XX
PF 04-JUN-2001; 2001US-0295607P.
PR 04-JUN-2001; 2001US-0295661P.
PR 06-JUN-2001; 2001US-0296404P.
PR 06-JUN-2001; 2001US-0296418P.
PR 11-JUN-2001; 2001US-0297414P.
PR 12-JUN-2001; 2001US-0297567P.
PR 14-JUN-2001; 2001US-0298285P.
PR 15-JUN-2001; 2001US-0298556P.
PR 21-JUN-2001; 2001US-0299949P.
PR 26-JUN-2001; 2001US-0300883P.
PR 28-JUN-2001; 2001US-0301550P.
PR 13-AUG-2001; 2001US-0311972P.
PR 27-AUG-2001; 2001US-0315069P.
PR 27-AUG-2001; 2001US-0315071P.
PR 29-AUG-2001; 2001US-0315660P.
PR 14-SEP-2001; 2001US-0322293P.
PR 17-SEP-2001; 2001US-0322706P.
PR 14-DEC-2001; 2001US-0341186P.
PR 28-FEB-2002; 2002US-0361189P.
PR 12-MAR-2002; 2002US-0363673P.
PR 12-MAR-2002; 2002US-0363676P.
XX
(ANDE/) ANDERSON D W.
PA (BAUM/) BAUMGARTNER J C.
PA (BOLD/) BOLD OG F L.
PA (CASW/) CASMAN S J.
PA (EDIN/) EDINGER S R.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUOX/) GUO X S.
PA (HJAL/) HJALT T.
PA (KEKU/) KEKUDA R.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALV/) MALVANKAR U M.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.

PA (PENA/) PENA C E A.
PA (RST/) RASTELLI L.
PA (SHIM/) SHIMKETS R A.
PA (STON/) STONE D J.
PA (SPYT/) SPYTEK K A.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.
XX
XX Anderson DW, Baumgartner JC, Boldog FL, Casman SJ, Edinger SR;
PI Gangolli EA, Gerlach V, Gorman L, Guo XS, Hjalt T, Kekuda R, Li L;
PI MacDougall JR, Malvankar UM, Millet I, Padigaru M, Patturajan M;
PI Pena CE, Rastelli L, Shinkets RA, Stone DJ, Spytek KA, Vernet CM;
PI Voss EZ, Zernhusen BD;
XX
XX WPI; 2004-090456/09.
DR N-PSDB; ADM93874.
XX
XX New NOVX polypeptide, useful for preparing a composition for treating or
PT preventing e.g., cancer, neurodegenerative disorders such as Parkinson's
PT disease, or metabolic disorders such as diabetes or obesity, or for
PT tissue typing.
XX
XX Claim 1; SEQ ID NO 94; 202pp; English.
XX
XX The invention relates to an isolated NOVX polypeptide. The polypeptide is
CC useful for preparing a composition for treating or preventing a pathology
CC associated with NOVX polypeptide e.g. cancer, neurodegenerative disorders
CC such as Parkinson's disease, metabolic disorders such as diabetes or
CC obesity or immune related disorders or for tissue typing. The present
CC sequence represents a human NOV protein.
XX
XX Sequence 582 AA;

Query Match 38.2%; Score 1193.5; DB 8; Length 582;
Best Local Similarity 45.5%; Pred. No. 1.2e-78;
Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;

QY 1 MLLWVLLVLPVSGQFARTPRPIIPLQPPWTVFGGERVTLTKGFRYSQ-KTKWYH 59
DB 1 MLLWLLLLITLTPGREGSGVAPKAVLLNPPWSTAFKGEKVALICSSISHLAQGGTYWYH 60

QY 60 RYLKREILRETPDNILOVEGSEYRCQAGSPSSPVHLDFSSASLILQAPLSVFEQDSV 119
DB 61 ----DEKLLIKHKDKI-QITEPGNYCKTKGSSLSDAVHVEFPDWLILQALHPVFGDNV 116

QY 120 VLRCAKAEVTLNNTIYKNDNLVAFLNKRTDPhiPHACLKNGAYRCTGYKSC---CPV 176
DB 117 ILRCQCKDNKNTHQVYKDGKQLPNSYNLEKITVNSVRDNSKYHCTAYRKPFYILDIEV 176

QY 177 SNTVKIQVEPTTRVLRASSFPQISGNPVTLCETQSLERSDYLFRFRFRDDQTLG 236
DB 177 TSXPLNIQVQLFLHPVLRASSFTPIEGSHPTLTCTQLSPQRPDVLQSFSLFRDSQTLG 236

QY 237 LGWSLSPNFOITAMWKGDSFYKCAATWPHSVISDSRPSWIOVQ-IPASHVPLVLTSPKX 295
DB 237 LGWSRSPRIQIPAMWTEDESSGYCEVETVTHSIKKSLSQIEVQRPVSNVNLRTPTG 296

QY 296 ALNFEGTKVTLHCETQEDSLRTLYRPHYHGVPLRHKSVCRCGASISFSLTT---ENSGN 352
DB 297 GOLIEGNMVLICSAVAGSGTFTFSWHKEG-RVRSGLRKTQRLSLLAEHLVLTVKESDAGR 355

QY 353 YCTADNGLCAKSKAVLSVTVPVSHVPLNLSPEDLIFEGAKVTLHCEAORGSPILY 412
DB 356 YCAADNVHSPILSTWIRVTRIPVSHVPLTFRAPRAHTVVGDLLEHCELSRGSPILY 415

QY 413 QPHHEAALERRRANGAGGVAISFSLTAESGNYCTADNGFGPQRSKAVLSITVPVSH 472
DB 416 RFYHEDVTLNGNSAPSGGGASFNLSLTAESGNYSCDADNGLGAQSHGSLRVTPVSR 475

QY 473 PVLTLSAEALTEGATVTLHCEVQSGSPQILYQFHEDMPLVSSSTPVSGRVSFSLIT 532
DB 476 PVLTLRAPGAQAVVGDLLEHCELSRGSPFILYFWFYHEDDTLGNISAHSGGGASFNLSLT 535

QY 533 EGHSGNYCTADNGFGPQRSEWSLFTVTG 561
DB 536 TEHSGNYSCDADNGLGAQSHKSVTLNVTG 564

RESULT 12
ADM06089
ID ADM06089 standard; protein; 707 AA.
XX
AC ADM06089;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human protein of the invention SEQ ID NO:4774.
XX
KW human; gene therapy; diagnostic marker; pharmaceutical.
XX
OS Homo sapiens.
XX
FN EP1347046-A1.
XX
PD 24-SEP-2003.
XX
PF 12-APR-2002; 2002EP-00008400.
XX
PR 22-MAR-2002; 2002JP-00137785.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-723558/69.
DR N-PSDB; ADM03646.
XX
XX New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX
PS Claim 1; SEQ ID NO 4774; 305pp; English.
XX
XX The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention ADM06202-ADM06773 is useful
CC therapy. An oligonucleotide of the invention ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM0316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC protein sequence of the invention.
XX
SQ Sequence 707 AA;

Query Match 38.2%; Score 1193.5; DB 7; Length 707;
Best Local Similarity 45.5%; Pred. No. 1.5e-78;
Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;

QY 1 MLLWVLLVLPVSGQFARTPRPIIPLQPPWTVFGGERVTLTKGFRYSQ-KTKWYH 59
DB 1 MLLWLLLLITLTPGREGSGVAPKAVLLNPPWSTAFKGEKVALICSSISHLAQGGTYWYH 60

QY 60 RYLKREILRETPDNILOVEGSEYRCQAGSPSSPVHLDFSSASLILQAPLSVFEQDSV 119
DB 61 ----DEKLLIKHKDKI-QITEPGNYCKTKGSSLSDAVHVEFPDWLILQALHPVFGDNV 116

QY 120 VLRCAKAEVTLNNTIYKNDNLVAFLNKRTDPhiPHACLKNGAYRCTGYKSC---CPV 176
DB 117 ILRCQCKDNKNTHQVYKDGKQLPNSYNLEKITVNSVRDNSKYHCTAYRKPFYILDIEV 176

QY 177 SNTVKIQVEPTTRVLRASSFPQISGNPVTLCETQSLERSDYLFRFRFRDDQTLG 236

[illegible]

RESULT 13

AAB82316
ID AAB82316 standard; protein; 734 AA.

AA
AC AAB82316;

DT 23-JUL-2001 (first entry)

DE Human immunoglobulin receptor IRTA3 protein.

Immunoglobulin superfamily receptor translocation associated; IRTA3;
human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma; myeloma;
B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.
XX
OS Homo sapiens.

XX
PN
WO200138490-A2.

PD 31-MAY-2001.

28-NOV-2000; 2000WO-US032403.

PR 29-NOV-1999; 99US-0168151P.

PA (UYCO) UNIV COLUMBIA NEW YORK.

Dalla-Favera R;

WPI; 2001-355921/37.

DR N-PSDB; AAF30953.

New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor Translocation Associated proteins, used to treat B cell malignancies including lymphomas and multiple myeloma.

PS Claim 4; Fig 18C-1-18C-2; 72pp; English.

The present sequence is that of the novel human immunoglobulin receptor, immunoglobulin superfamily receptor translocation associated protein 3 (IRTA3), an FC receptor involved in the pathogenesis of lymphoma and melanoma. Efforts to identify genes involved in chromosomal aberrations affecting band Ig21 in multiple myeloma and B cell lymphoma led to the discovery of IRTA1 and IRTA2 (see AAB82312-15) as founding members of a novel subfamily of related receptors within the immunoreceptor family. 3 Additional proteins, IRTA3, IRTA4 and IRTA5 (see AAB82316-18), were

DE Human LY1448P cancer related protein for cancer detection method.

XX cytostatic; T-cell vaccine; detection; cancer;
KW chronic lymphocytic leukemia.

XX Homo sapiens.

XX WO2003077836-A2.

XX 25-SEP-2003.

XX 06-NOV-2002; 2002WO-US035728.

XX 06-NOV-2001; 2001US-00040862.

XX 23-MAY-2002; 2002US-00154884.

XX (CORI-) CORIXA CORP.

XX Gaiger A, Algate PA, Mannion J, Retter M;

XX WPI; 2003-756941/71.

XX Detecting cancer in a patient comprises contacting a biological sample
PT from the patient with a binding agent that binds to a cancer-associated
PT polypeptide and comparing the amount of polypeptide to a predetermined
PT cutoff value.

XX Disclosure; SEQ ID NO 10463; 419pp; English.

XX The invention relates to a method of detecting (M1) cancer in a patient
CC by: (i) contacting a biological sample from the patient with an agent
CC that binds to any of three polypeptides given in the specification; (ii)
CC detecting in a sample an amount of the peptide that binds to the binding
CC agent; and (iii) comparing the amount of polypeptide present in the
CC patient's sample to a predetermined cutoff value. The specification also
CC discloses a separate method for detecting (M2) cancer in a patient by a
CC method similar to M1, except that the detection agent is an
CC oligonucleotide that binds to any of three polynucleotides given in the
CC specification. M1 and M2 are useful for detecting the presence of cancer
CC in a patient, especially chronic lymphocytic leukemia. The applicants
CC have identified specific human polypeptides overexpressed in one or more
CC types of hematological malignancies. This sequence corresponds to a
CC protein used in the method of the invention.

XX Sequence 734 AA;

Query Match 38.2%; Score 1193.5; DB 7; Length 734;

Best Local Similarity 45.5%; Pred. No. 1.6e-78;

Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;

QY 1 MLLWILLVLAVPSGQFARTPRPIIFLOPPMTTFQGERVTLTCKGFRFYSPO-KTKVWH 59

DB 1 MLLWILLVLITGRQSGVAPKAVALLNPNWSTAFKGEKVALICSIHSLAQGTYYWH 60

QY 60 RYLKGEILRETPDNLILEVOESGEYRCQAGSPFLSPVHLDPSSALILQAPLSVFGDSV 119

DB 61 ---DEKLLIKHKDKI-QITEPGNYCKTRGSSLSDAVHVPSPDMLILQALHPVEGDNV 116

QY 120 VLRCRAKAEVTLNNTYKNDVLAFLNKRTDHHIIPACLKONGAYRCTGYKESC---CPV 176

DB 117 ILRCQKGNKNTKQVYKDGQLENSVNLKXITVNSVSRDMSKYHAYRKFYILDIEV 176

QY 177 SSNTVKIOVEPFTRPVLRASSFQPIISGNPVTCTQSLERSVPLRFRFRDDQTLG 236

DB 177 TSKPNIQVQELFLHPVLRASSSTIEGSPMTLTCTQLSPQPDVQVQSLFRDSQTLG 236

QY 237 LGWSLSPNQITAMWSKDSGFYCKAAATMPHSVIDSPRSWTQVQ-IPASHVPLTISPEK 295

DB 237 LGWSRSPRLQIPAMWTEDSGSVCEVETVTHSIKRSLSRQLRVQVPSNVNLEIRPTG 296

QY 296 ALNFGTKVTLHCETQEDSLRLTYRFGYHGVPLRHKSVRCERGASISFLIT---ENSGN 352

DB 297 GOLIEGNNMVLICSAVQAQSGTGTTFGSMHKEG-KVRSLSGRKTQRSLLAELHLVLTVESDAGR 355

QY 353 YYCTADNGLGAKPSKAVSLSVTPVSPVHPVLNLSPPEDLIFEGAKVTLHCEAQRGSLPTLY 412

DB 356 YICADNVHSPILSTWIRVIRPVPVLPVTRAPVTVVGDLELHCELRGSPPIY 415

QY 413 OFHEDAALERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRKAVSLISITVPVSH 472

DB 416 RPYHEDVTILGNSSAPSGGASFNLSLTAHSGNYSKCDADNGLGAQHSHGVSLRVTPVSR 475

QY 473 PVLTLSSAEALTFFGATVTLHCEVQSGPQLLYQPHYHEDMPLVSSSTPSVGRVSFSLIT 532

DB 476 PVLTLRAPGAQVAVVGDLELHCELRGSPPIYLYFYHEDDTLGNISAHSGGASFNLSL 535

QY 533 ECHSGNYYCTADNGFGPQRSEVSLFVTG 561

DB 536 TEHSGNYSCEADNGLGAQHSHGVSLRVTVNG 564

RESULT 15

ABM84916

ID ABM84916 standard; protein; 750 AA.

XX AC ABM84916;

XX DT 18-NOV-2004 (first entry)

XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:5165.

XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX OS Homo sapiens.

XX PN WO2004023973-A2.

XX PD 25-MAR-2004.

XX PF 12-SEP-2003; 2003WO-US028227.

XX PR 12-SEP-2002; 2002US-0410259P.

XX PR 12-SEP-2002; 2002US-0410260P.

XX PA (INCY-) INCYTE CORP.

XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Bldier LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EU, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtan ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patuary S, Shi X, Suarez CJ;
XX WPI; 2004-329368/30.
DR N-PSDB; ACN43568.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

XX PS Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide

CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithio protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 750 AA;

```
Query Match      38.2%; Score 1193.5; DB 8; Length 750;
Best Local Similarity 45.5%; Pred. No. 1.7e-78;
Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;

Qy 1 MLLWVILLVLPASGQFAPTRPIIFLPQWTVTFQGERVTLCKGRFRFYSPQ-KIKWYH 59
Db 1 MLLWVILLVLPASGQFAPTRPIIFLPQWTVTFQGERVTLCKGRFRFYSPQ-KIKWYH 59
Qy 60 RYLKKEITRETPDNILVQESGEYRCAQGSPLSSPVHLDPFSSASLILQAPLSVFEGDSV 119
Db 61 ---DEKLLKIKHDKI-QITEFGNYQCKTRGSSLSDAVHVEFSPDWLLILQALHPVFEQDNV 116
Qy 120 VLRCRAKAEVTLNNTIYKNDNVLAFLNKRTRDFHPIHACLKDNAGYRCTGYKESC---CPV 176
Db 117 ILRCQKDNKNTKQVYKQKQLPNSYNLEKITVNSVRDNSKYCHTAIRKFVILDIEV 176
Qy 177 SSNTVKIQVQEPFTRPVLRASSFOISGNPVTLTCETQLSLERSDVPFRFRDDQTLG 236
Db 177 TSKPLNIQVQELFLHPVLRASSPTIEGSPMTLTCTQLSPQRPDVQLQPSLFRDSQTLG 236
Qy 237 LGWSLSPNFOITAMWSKDSGFYCKAATMPHSVTSDSFRSWIQVO-IPASHPVLTLSPEX 295
Db 237 LGWSRSPRLQIPAMWTEDESGSYWCEVETVTHSIKKRSLRQIRVQRPVPSNVNLEIRPTG 296
Qy 296 ALNPEGTVTLHCETQSDSLRTLYRFYHEGVPLRHKSVRCERGASISFSLT---ENSGN 352
Db 297 GQLIEGENMVLICSAQSGTVTFSEWKEG-RVRSIGRKTQRSLLAEHLVLTVKESDAGR 355
Qy 353 YYCTADNGLGAKPSKAVSLVTVVPVSHPVNLNLSPEDLIFEGAKVTLHCEAQRGSLPILY 412
Db 356 YYCAADNVHSPILSTWIRVTIRIPVSHPVLTFRAPRAHTVVGDLLELHCESLRGSPILY 415
Qy 413 QFHEDAALEERSNANSAGGVAISFSLTAHSGNYCTADNFGFGPQORSKAVSLITVPVSH 472
Db 416 RFYHEDVTLGNSSAPSGGGASFNLSLTAHSGNYSCDADNGLGAQSHGSLRVTVPVSR 475
Qy 473 PVLTLSSAEALTPEGATVTLHCEVQSGPQILYOFYHEDMPLVSSSTPSVGRVSFSPSLT 532
Db 476 PVLTLRAPGAQAVVGDLELHCESLRGSPILYWFYHEDDTLGNISAHSGGGASFNLSLT 535
Qy 533 EHGSGNYCTADNFGFGPQSEVSLFVTG 561
Db 536 TEHSGNYSCDADNGLGAQSHKVTNLNVTG 564
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Search completed: May 4, 2005, 11:32:40
Job time : 80.2887 secs

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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:27:40 ; Search time 19.8351 Seconds
(without alignments)
2227.987 Million cell updates/sec

Title: US-09-724-254A-3

Perfect score: 3124

Sequence: 1 MLLWVILLVLPVSGQFART.....AEFSLTHFKNLPALSSFLP 592

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2953	94.5	1248	4	US-09-949-016-10595
2	2953	94.5	1248	4	US-09-949-016-10596
3	386	12.4	261	4	US-09-245-764-7
4	305.5	9.8	254	2	US-08-667-939A-3
5	305.5	9.8	254	4	US-08-433-123-3
6	304.5	9.7	254	2	US-08-667-939A-2
7	304.5	9.7	254	4	US-08-433-123-2
8	299.5	9.6	4391	4	US-10-006-011A-2
9	293	9.4	233	2	US-08-667-939A-6
10	293	9.4	233	4	US-08-433-123-6
11	292.5	9.4	254	2	US-08-667-939A-9
12	292.5	9.4	254	4	US-08-433-123-9
13	292	9.3	233	2	US-08-667-939A-5
14	292	9.3	233	2	US-08-667-939A-8
15	292	9.3	233	4	US-08-433-123-5
16	292	9.3	233	4	US-08-433-123-8
17	290	9.3	315	4	US-09-949-016-11121
18	290	9.3	315	4	US-09-949-016-11122
19	288.5	9.2	254	2	US-08-667-939A-4
20	288.5	9.2	254	4	US-08-433-123-4
21	286	9.2	233	2	US-08-667-939A-7
22	286	9.2	233	4	US-08-433-123-7
23	285.5	9.1	254	2	US-08-667-939A-1
24	285.5	9.1	254	4	US-08-433-123-1
25	275	8.8	197	3	US-08-788-954-2
26	275	8.8	203	2	US-08-667-939A-20
27	275	8.8	203	4	US-08-433-123-20

28	274	8.8	174	4	US-09-245-764-8	Sequence 8, Appli
29	271	8.7	215	2	US-08-667-939A-18	Sequence 18, Appl
30	271	8.7	215	4	US-08-433-123-18	Sequence 18, Appl
31	269.5	8.6	199	2	US-08-768-964-12	Sequence 12, Appl
32	269.5	8.6	199	3	US-09-005-299-12	Sequence 12, Appl
33	269.5	8.6	199	3	US-09-515-431-12	Sequence 12, Appl
34	269.5	8.6	263	2	US-08-768-964-2	Sequence 2, Appli
35	269.5	8.6	263	3	US-09-005-299-2	Sequence 2, Appli
36	269.5	8.6	263	3	US-09-515-431-2	Sequence 2, Appli
37	267	8.5	197	2	US-08-756-387B-11	Sequence 11, Appl
38	267	8.5	197	3	US-09-285-873-11	Sequence 11, Appl
39	267	8.5	197	3	US-09-944-277A-11	Sequence 11, Appl
40	267	8.5	257	1	US-07-869-933-11	Sequence 11, Appl
41	267	8.5	257	2	US-08-756-387B-2	Sequence 2, Appli
42	267	8.5	257	3	US-09-103-663-11	Sequence 11, Appl
43	267	8.5	257	3	US-09-285-873-2	Sequence 2, Appli
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45	267	8.5	257	4	US-09-944-277A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-949-016-10595
; Sequence 10595, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10595

; LENGTH: 1248

; TYPE: PRT

; ORGANISM: Human

; US-09-949-016-10595

Query Match 94.5%; Score 2953; DB 4; Length 1248;

Best Local Similarity 97.9%; Pred. No. 7.8e-260;

Matches 562; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MLLWVILLVLPVSGQFARTPRDIIIFLOPPWTVFQGERVTLTKGFRFYSPQTKWYHR 60

DB 476 MLLWVILLVLPVSGQFARTPRDIIIFLOPPWTVFQGERVTLTKGFRFYSPQTKWYHR 535

QY 61 YLCKEILRETPDNILEVQSGEYRCQAQSPVHLDFSSASLILQAPLSVFEQSVV 120

DB 536 YLCKEILRETPDNILEVQSGEYRCQAQSPVHLDFSSASLILQAPLSVFEQSVV 595

QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHAPHACKLNDGAYRCTGYKESCCPVSSNT 180

DB 596 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHAPHACKLNDGAYRCTGYKESCCPVSSNT 655

QY 181 VKIQVQEPFTRPVLRASSQPIISGNPVTLTCTQLSLERSDVLRRFRFRDDQTLGLGWS 240

DB 656 VKIQVQEPFTRPVLRASSQPIISGNPVTLTCTQLSLERSDVLRRFRFRDDQTLGLGWS 715

QY 241 LSPNFOITAMWSKDSGFYCKAATMPHSVTSDSPRSIQVQIPASHPVLTLSPKALNFE 300

DB 716 LSPNFOITAMWSKDSGFYCKAATMPHSVTSDSPRSIQVQIPASHPVLTLSPKALNFE 775

QY 301 GTKVTLHCETQEDSLRFLRYFYHEGVPLRHKSVRCRGASISFSLTTENSNGNYCTADNG.360

361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA 420
 836 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA 895
 421 LERRANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
 896 LERRANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 955
 481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPSVGRVSPFSFSLTEGHSNGY 540
 956 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPSVGRVSPFSFSLTEGHSNGY 1015
 541 CTADNGFGPQRSEVSLFVTGKCVLASKPPLAE 574
 1016 CTADNGFGPQRSEVSLFVTGKCVLASKPPLAE 1049

RESULT 3
 US-09-245-764-7
 ; Sequence 7, Application US/09245764
 ; Patent No. 6675105
 ; GENERAL INFORMATION:
 ; APPLICANT: Hogarth, P. Mark
 ; APPLICANT: Powell, Maree S.
 ; APPLICANT: McKenzie, Ian F.C.
 ; APPLICANT: Maxwell, Kelly F.
 ; APPLICANT: Garrett, Thomas P.J.
 ; APPLICANT: Epa, Vidana
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF FC RECEPTORS
 ; FILE REFERENCE: 4102-4
 ; CURRENT APPLICATION NUMBER: US/09/245,764
 ; CURRENT FILING DATE: 1999-02-05
 ; EARLIER APPLICATION NUMBER: 60/099,994
 ; EARLIER FILING DATE: 1998-09-11
 ; EARLIER APPLICATION NUMBER: 60/073,972
 ; EARLIER FILING DATE: 1998-02-06
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 261
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; ORGANISM: Homo sapiens
 ; US-09-245-764-7

Query Match 12.4%; Score 386; DB 4; Length 261;
 Best Local Similarity 35.7%; Pred. No. 6.7e-27;
 Matches 95; Conservative 40; Mismatches 121; Indels 10; Gaps 6;
 20 TPRPIIFLOPPMTTVFQGERVTLCKGPRFYSPOKTKWYHYLKGKILRETPD--NILE 76
 1 TTKAVITLQPPMVSVFQETVTLHCEVHLPGSSSTQWVFN--GTATQSTPSYRITSAS 58
 77 VOESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVF-EGDSVVLRCRAKAEVTLNNTI 135
 59 VNSGEYRCQGLSGRSDPQLQEIHRGWLQLQVSRVFTGEPELALRCHAWKDLVYNVL 118
 136 YKNDNVLAFLNKRTPHIFACLDKNGAYRCTGYKESCCPVSSNTVKIQVOEPFTRPVLR 195
 119 YRNGKFKFHHNSNLTKTNISHNGTYHCSCGMKH--RYTSAGISVTVKELFPAPVLN 176
 196 ASSFPQ-ISGNPVTLCETQLSLERSDVPLRFRFRDQTLGLGWSLSPNFOITAMWSKD 254
 177 ASVTSPLLEGNLVTLSCTETKLLKQRPGLQLYFSFYMGSKTL-RGNTSSEYQILFARRED 235
 255 SGFYWCKAAATMPHSVSDSPRSWIQV 280
 236 SGLYCEAATDGNLKRSPLELQV 261

RESULT 4
 US-08-667-939A-3
 ; Sequence 3, Application US/08667939A

776 GTKVTLHCETQEDSLRTLYRYHEGVPLRHKSVRCERGASISFSLTTENSNGNYCTADNG 835
 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA 420
 836 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA 895
 421 LERRANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
 896 LERRANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 955
 481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPSVGRVSPFSFSLTEGHSNGY 540
 956 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPSVGRVSPFSFSLTEGHSNGY 1015
 541 CTADNGFGPQRSEVSLFVTGKCVLASKPPLAE 574
 1016 CTADNGFGPQRSEVSLFVTGKCVLASKPPLAE 1049

RESULT 2
 US-09-949-016-10596
 ; Sequence 10596, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10596
 ; LENGTH: 1248
 ; TYPE: PRT
 ; ORGANISM: Human
 ; ORGANISM: Human
 ; US-09-949-016-10596

Query Match 94.5%; Score 2953; DB 4; Length 1248;
 Best Local Similarity 97.9%; Pred. No. 7.8e-260;
 Matches 562; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPMTTVFQGERVTLCKGPRFYSPOKTKWYHR 60
 476 MLLWVILLVAPVSGQFARTPRPIIFLOPPMTTVFQGERVTLCKGPRFYSPOKTKWYHR 535
 61 YLKGKILRETPDNILEVOESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVPEGDSVV 120
 536 YLKGKILRETPDNILEVOESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVPEGDSVV 595
 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLDKNGAYRCTGYKESCCPVSSNT 180
 596 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLDKNGAYRCTGYKESCCPVSSNT 655
 181 VKIQVOEPFTRPVLRASSPQISGNPVTLCETQLSLERSDVPLRFRFRDQTLGLGWS 240
 656 VKIQVOEPFTRPVLRASSPQISGNPVTLCETQLSLERSDVPLRFRFRDQTLGLGWS 715
 241 LSPNFOITAMWSKDSGFYWCKAAATMPHSVSDSPRSWIQVLPASHPVLTLSPEKALNFE 300
 716 LSPNFOITAMWSKDSGFYWCKAAATMPHSVSDSPRSWIQVLPASHPVLTLSPEKALNFE 775
 301 GTKVTLHCETQEDSLRTLYRYHEGVPLRHKSVRCERGASISFSLTTENSNGNYCTADNG 360
 776 GTKVTLHCETQEDSLRTLYRYHEGVPLRHKSVRCERGASISFSLTTENSNGNYCTADNG 835

```
; Patent No. 5998166
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/667,939A
; FILING DATE: 24-JUN-1996
; PRIOR APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO=2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-667-939A-3

Query Match 9.8%; Score 305.5; DB 2; Length 254;
Best Local Similarity 32.9%; Pred. No. 1.4e-19;
Matches 91; Conservative 37; Mismatches 102; Indels 47; Gaps 11;

Qy 1 MLLVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTKGFRFYSPQ--KTKWY 58
   ||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 LLLPTALLLVASAGMRTEDLPKAVFLEPQWYRVLEKDSVTLKCG--AYSPEDNSTQWF 61
   ||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 59 HRYLGKEILRETPDNILE-----VQSGEYRCQAQSGPLSSPHLDFSSASLI 106
   ||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 HK-----ENLISSQAASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEVQVGWLL 110
   ||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 107 LQAPLSVF-EGDSVWLRCRAKAEVTLNNTIY-KDNVLAFLNKRTDPHIFACIKONGAY 164
   ||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 111 LQAPRWFKEDPIHLRCHSWKNTALHKVYTLQNGDKRKYFHNSDPHIFKATLKDSGSY 170
   ||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 165 RCTGYKESCCPVSSNTVKIQVQEPFTRPVLRASSFQPSIGNPVTLTCTETSLERSDVPL 224
   ||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 171 FCRGLVGS-KNVSETVNIITQGLA--VSTISSFFP-PGYQVSF-CLVMVLLFAVDT-- 223
   ||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 225 RFRFRDDQTLGLGWSLSPNFQITAMWSKDSGFYCK 261
   ||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 224 -----GLYFSVKTNIRSTRDKDHPKRWK 249
   ||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
US-08-433-123-3
; Sequence 3, Application US/08433123
; Patent No. 644789
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:

; Patent No. 5998166
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/667,939A
; FILING DATE: 24-JUN-1996
; PRIOR APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO=2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-667-939A-3

Query Match 9.8%; Score 305.5; DB 2; Length 254;
Best Local Similarity 32.9%; Pred. No. 1.4e-19;
Matches 91; Conservative 37; Mismatches 102; Indels 47; Gaps 11;

Qy 1 MLLVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTKGFRFYSPQ--KTKWY 58
   ||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 LLLPTALLLVASAGMRTEDLPKAVFLEPQWYRVLEKDSVTLKCG--AYSPEDNSTQWF 61
   ||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 59 HRYLGKEILRETPDNILE-----VQSGEYRCQAQSGPLSSPHLDFSSASLI 106
   ||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 HK-----ENLISSQAASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEVQVGWLL 110
   ||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 107 LQAPLSVF-EGDSVWLRCRAKAEVTLNNTIY-KDNVLAFLNKRTDPHIFACIKONGAY 164
   ||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 111 LQAPRWFKEDPIHLRCHSWKNTALHKVYTLQNGDKRKYFHNSDPHIFKATLKDSGSY 170
   ||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 165 RCTGYKESCCPVSSNTVKIQVQEPFTRPVLRASSFQPSIGNPVTLTCTETSLERSDVPL 224
   ||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 171 FCRGLVGS-KNVSETVNIITQGLA--VSTISSFFP-PGYQVSF-CLVMVLLFAVDT-- 223
   ||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 225 RFRFRDDQTLGLGWSLSPNFQITAMWSKDSGFYCK 261
   ||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 224 -----GLYFSVKTNIRSTRDKDHPKRWK 249
   ||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
US-08-667-939A-2
; Sequence 2, Application US/08667939A
; Patent No. 5998166
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,939A
FILING DATE: 24-JUN-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/433,123
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LUO=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-667-939A-2

Query Match 9.7%; Score 304.5; DB 2; Length 254;
Best Local Similarity 32.9%; Pred. No. 1.7e-19;
Matches 91; Conservative 38; Mismatches 101; Indels 47; Gaps 11;
QY 1 MLLWVILLVLPVSGGFQPARTPRPIIFLOPPWTTVFOGERVTLTKGFRFYSPQ--KTKWY 58
Db 4 LLLPTALLLVASGMRTEPLKAVFLEPQWYSLVKDSVTLKCOG--AYSPEDNSTQWF 61
QY 59 HRYLGKILRETPDNILE-----VQSSGEYRCQAQSPSSPLSSPVHLDFFSSASLI 106
Db 62 HK-----ENLISSQASSYFIDAATVDSGEYRCQTNLSTLSDPVQLEVQVQWLL 110
QY 107 LOAPLSVF-EGDSVVLRCRAKAEVTLNNTTY-KNDNVLAFLNKRTPDHPHACLKNGAY 164
Db 111 LOARWVFKEDPIHLACHSWKNTALHKVTYLONGKDRKYFHNSDFHHPKATLKDSGSY 170
QY 165 RCTGKSCCPSVNTVKIQVQEFTRPVLRASSFQIPISGNPVTLTCTETSLERSDVPL 224
Db 171 FCKGLVGS-KNVSETVNTIIOGLA--VSTNSFFP-PGYQVSF-CLVNVLLFAVDT-- 223
QY 225 RFRFRDDQTLGLGWSLSPNFQITAMWSKDSGFYCK 261
Db 224 -----GLYFSVKTNRSTRDWKDKHFKWKR 249

RESULT 7
US-08-433-123-2
Sequence 2, Application US/08433123
Patent No. 6444789
GENERAL INFORMATION:
APPLICANT: LUO, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,123

FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LUO=2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-123-2

Query Match 9.7%; Score 304.5; DB 4; Length 254;
Best Local Similarity 32.9%; Pred. No. 1.7e-19;
Matches 91; Conservative 38; Mismatches 101; Indels 47; Gaps 11;
QY 1 MLLWVILLVLPVSGGFQPARTPRPIIFLOPPWTTVFOGERVTLTKGFRFYSPQ--KTKWY 58
Db 4 LLLPTALLLVASGMRTEPLKAVFLEPQWYSLVKDSVTLKCOG--AYSPEDNSTQWF 61
QY 59 HRYLGKILRETPDNILE-----VQSSGEYRCQAQSPSSPLSSPVHLDFFSSASLI 106
Db 62 HK-----ENLISSQASSYFIDAATVDSGEYRCQTNLSTLSDPVQLEVQVQWLL 110
QY 107 LOAPLSVF-EGDSVVLRCRAKAEVTLNNTTY-KNDNVLAFLNKRTPDHPHACLKNGAY 164
Db 111 LOARWVFKEDPIHLACHSWKNTALHKVTYLONGKDRKYFHNSDFHHPKATLKDSGSY 170
QY 165 RCTGKSCCPSVNTVKIQVQEFTRPVLRASSFQIPISGNPVTLTCTETSLERSDVPL 224
Db 171 FCKGLVGS-KNVSETVNTIIOGLA--VSTNSFFP-PGYQVSF-CLVNVLLFAVDT-- 223
QY 225 RFRFRDDQTLGLGWSLSPNFQITAMWSKDSGFYCK 261
Db 224 -----GLYFSVKTNRSTRDWKDKHFKWKR 249

RESULT 8
US-10-006-011A-2
Sequence 2, Application US/10006011A
Patent No. 6821947
GENERAL INFORMATION:
APPLICANT: Iozzo, Renato V.
TITLE OF INVENTION: Endorepellin: methods and compositions
TITLE OF INVENTION: for inhibiting angiogenesis
FILE REFERENCE: 8321-95
CURRENT APPLICATION NUMBER: US/10/006,011A
CURRENT FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 4391
TYPE: PRT
ORGANISM: human
US-10-006-011A-2

Query Match 9.6%; Score 299.5; DB 4; Length 4391;
Best Local Similarity 23.5%; Pred. No. 4e-17;
Matches 145; Conservative 90; Mismatches 264; Indels 117; Gaps 28;
QY 23 PIIFLOPPWTTVFOGERVTLTKGFRFYSPQK-TKWYHYLGKELRETPDNIL-----E 76
Db 2630 PPRIESSPTVEGGQTLDCNCVWAR-QPQALITWKGGSLPSRHQTHGSHLHQMS 2687
QY 77 VQSSGEYRCQAQ-----GSP-----LSSPVHLDFFSSASLILOAPLSVF 114

Db 2688 VADSGEYVCRANNIDALEASIVISVSPSAGSPAGSSMEIRIESSS-----HVA 2739
Qy 115 EGD5VWLCRAKAEVTLNNTIYKNDNVLA--FLNKRDTDFHIPHACLKNDGAYRC-----T 167
Db 2740 EGETDLNCVVPQAHQAQVTHKRGSLPSHHQTRGSRRLRHVSPADSGEYVCRVMGSS 2799
Qy 168 GYKESCCPV-----SNTVKIQVBEPTFRVLK--ASSFQIPISGNPVTLTC-----ETQLS 216
Db 2800 GPLEASVLTVEASGSAVHPAPGAPPIRIEPPSSRVARSGQTLDLKCVVPQAHQAQVT 2859
Qy 217 LER--SDVPLRFRFRDDQTLGLGWSLSPNFQITAMWSKDSGFYWK-----AATMPSHV- 269
Db 2860 WHKGGNLPARHGVH-----GPLRLNQVSPADSGEYSCQVTGSSGTLEASVL 2907
Qy 270 ISDSPRWIQVQIPASHPVLTLSPEKALNPEGTQVTLHCETQEDSLRTLRFYHEG--VP 327
Db 2908 VTIEPSPGPPIAPGLAQPIVIEASSHVTEGQTLDLNCVVPQA-HAQVTWYKRGSLP 2966
Qy 328 LRKHSVRCERGASISFSLTT-ENSGNYCTADNGLGAKPKANVLSLTVTPVSH----- 379
Db 2967 ARHQT-----HGSQLRLHVSADSGEYVCRASGPG--PEQASFTVTPPSEGSYRLR 3020
Qy 380 -PVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHHEDAALERRSANSAGGVAISFSL 438
Db 3021 SPVISEDPPSTVOQQDASFCKLIHGAAPISLEWTRNQLELDNVHISPNGSIITVIG 3080
Qy 439 T-AEHSNGNYCTADNFGPQSKAVLSITVPVSHPVLTLSABALTFEGATVTLHCEVQ 497
Db 3081 TRPSNHGTYRCVASNAYVAQS--VNL5VHGPTT--VSVLPEGVPVWVKAVTLEC-VS 3136
Qy 498 RGSPOILYQFHEMDPLVSSSTPSVGRVSFSFSLTEGH-----SGNYCTADN 545
Db 3137 AGEPRSSARWTR-----ISSTPA-KLEQRTYGLMDSHAVLIQISAKPDSAGTYVCLAQN 3189
Qy 546 GFGPQRSEVWSLFTVG 561
Db 3190 ALGTAQKQVEVVDTG 3205

RESULT 9
US-08-667-939A-6
; Sequence 6, Application US/08667939A
; Patent No. 5998166
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,939A
; FILING DATE: 24-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO=2A
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-667-939A-6

Query Match 9.4%; Score 293; DB 2; Length 233;
Best Local Similarity 34.7%; Pred. No. 1.7e-18;
Matches 84; Conservative 32; Mismatches 92; Indels 34; Gaps 10;

Qy 1 MLMLVILLVLPVSGQFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSPQ--KTKWY 58
Db 4 LLLPTALLLVASGMRTEDLPKAVFLEPQWRYRLEKDSVTLKCGQ--AYSPEDNSTQWF 61
Qy 59 HRVILGKILRETPDNILE-----VOESGEYRCQAQGSPLASPVHLDFFSSASLI 106
Db 62 HN-----ENLISSQASSYFIDAATVDDSGEYRCQNLSTLSDPVQLEHVHVGWLL 110
Qy 107 LQAPLSVP-EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRDTDFHIPHACLKNDGAY 164
Db 111 LQAPRWVFKBEDPIHLRACHSKWKTALHKVTVYLONGKDRKYFHNSDFHIPKATLKDSGY 170
Qy 165 RCTGYKESCCPVSNVTVKIQVQBPFTPRVLRASSFPQISGNPVTLTCETQLSLERSDVL 224
Db 171 FCRGLVGS-KNVSSETVNITITOGLA--VSTISSFSP-PGYQVSF-CLVMVLLFAVDVTGL 225
Qy 225 RF 226
Db 226 YF 227

RESULT 10
US-08-433-123-6
; Sequence 6, Application US/08433123
; Patent No. 6444789
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,123
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO=2
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-433-123-6

Query Match 9.4%; Score 293; DB 4; Length 233;
Best Local Similarity 34.7%; Pred. No. 1.7e-18;
Matches 84; Conservative 32; Mismatches 92; Indels 34; Gaps 10;

QY 1 MLLWILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSQ--KTKWY 58
DB 4 LLLPTALLLVLSAGMRTEDLPKAVVFLFPQWYRVLEKDSVTLKCG--AYSPEDNSTQWF 61
QY 59 HRYLKGKILRETPDNIL-----VOESGEYRCQAQGSPLSPVHLDFFSSASLILOAPLSVF 114
DB 62 H--NESLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEVHIGWLLLOAPRWVF 118
QY 115 EGSVVLRCRAKAEVTLNNTIY-KDNVLAFLNKRDFHPIHACLKONGAYRCTGYKES 172
DB 119 KEEPIHLRCHSWKNTALHKVTYLONGKGRKYFHNSDFYIPKATLKDSGSYFCGLFGS 178
QY 173 CCPVSSNTVKIQVEPFRPVLRRASSFPISGNPVTLTCTQLSLERSDVPRLRFRPRDD 232
DB 179 -KNVSETVNITITQGLA--VSTISSFP-PGYQVSP-CLVMVLLFAVDT----- 223
QY 233 QTLGLWSLSPNFQITAMWSKDSGFYWK 261
DB 224 ---GLYFSVKTNIIRSTRDMKDKFKWRK 249

RESULT 12
US-08-433-123-9
; Sequence 9, Application US/08433123
; Patent No. 644789
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,123
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-433-123-9

Query Match 9.4%; Score 292.5; DB 4; Length 254;
Best Local Similarity 33.1%; Pred. No. 2.1e-18;
Matches 89; Conservative 38; Mismatches 111; Indels 31; Gaps 11;

QY 1 MLLWILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSQ--KTKWY 58
DB 4 LLLPTALLLVLSAGMRTEDLPKAVVFLFPQWYRVLEKDSVTLKCG--AYSPEDNSTQWF 61
QY 59 HRYLKGKILRETPDNIL-----VOESGEYRCQAQGSPLSPVHLDFFSSASLILOAPLSVF 114
DB 62 H--NESLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEVHIGWLLLOAPRWVF 118

Query Match 9.4%; Score 293; DB 4; Length 233;
Best Local Similarity 34.7%; Pred. No. 1.7e-18;
Matches 84; Conservative 32; Mismatches 92; Indels 34; Gaps 10;

QY 1 MLLWILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSQ--KTKWY 58
DB 4 LLLPTALLLVLSAGMRTEDLPKAVVFLFPQWYRVLEKDSVTLKCG--AYSPEDNSTQWF 61
QY 59 HRYLKGKILRETPDNIL-----VOESGEYRCQAQGSPLSPVHLDFFSSASLI 106
DB 62 HN-----ENLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEVHVGWLL 110
QY 107 LOAPLSVF-EGSVVLRCRAKAEVTLNNTIY-KDNVLAFLNKRDFHPIHACLKONGAY 164
DB 111 LOAPRWVFKEEPIHLRCHSWKNTALHKVTYLONGKDRKYFHNSDFYIPKATLKDSGSY 170
QY 165 RCTGYKESCCPVSSNTVKIQVEPFRPVLRRASSFPISGNPVTLTCTQLSLERSDVP 224
DB 171 FCRGLVGS-KNVSETVNITITQGLA--VSTISSFP-PGYQVSP-CLVMVLLFAVDIGL 225
QY 225 RF 226
DB 226 YF 227

RESULT 11
US-08-667-939A-9
; Sequence 9, Application US/08667939A
; Patent No. 5938166
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,939A
; FILING DATE: 24-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-667-939A-9

Query Match 9.4%; Score 292.5; DB 2; Length 254;
Best Local Similarity 33.1%; Pred. No. 2.1e-18;
Matches 89; Conservative 38; Mismatches 111; Indels 31; Gaps 11;

QY 1 MLLWILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSQ--KTKWY 58

QY 115 -EGDSVVLRCRAKAEVTLNNTIY-KNDNLVLAFLNKRDTDFHHPHACLKONGAYRCTGYKES 172
 Db 119 KEEDPIHLRCHSWKNTALHKVTVLQNGKGRKYFHNSDFYIPKATLKDSGSYFCRGLFGS 178
 QY 173 CCPVSSNTVKIQOEFTPRPVLRASSFPQISGNPVTLTCTETQLSLERSDVPLEFRFRDD 232
 Db 179 -KNVSETVNITITQGLA--VSTISSFSP-PGYQVSF-CLVMVLLFAVDTLGLYF 227
 QY 233 QTLGLWSLSPNFQITAMWKSOGFYWCK 261
 Db 224 --GLYSVKTNIRSTRDWDKHKFKWK 249
 RESULT 13
 US-08-667-939A-5
 ; Sequence 5, Application US/08667939A
 ; Patent No. 5998166
 ; GENERAL INFORMATION:
 ; APPLICANT: LUO, Shun
 ; TITLE OF INVENTION: CD16-II VARIANTS
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/667,939A
 ; FILING DATE: 24-JUN-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/433,123
 ; FILING DATE: 03-MAY-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROWDY, Roger L.
 ; REGISTRATION NUMBER: 25,618
 ; REFERENCE/DOCKET NUMBER: LUO-2A
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 233 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-667-939A-5
 Query Match 9.3%; Score 292; DB 2; Length 233;
 Best Local Similarity 35.5%; Pred. No. 2.1e-18;
 Matches 83; Conservative 34; Mismatches 99; Indels 18; Gaps 10;
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 Db 4 LLLPTALLLVLSAGMRTEDLPKAVVLEPQWYVLEKSDVTLKCG--AYSPEDNSTQWF 61
 QY 59 HRYLGEILRETDPNLT---EVOESGEYRCQAGSPPLSPVHLDFSSASLILOAPLSVF 114
 Db 62 H---NESLISSQASSYFIDAATVNDGSEYRCQNLSTLSDPVQVLEVHIGWLLQAPRWVF 118
 QY 115 -EGDSVVLRCRAKAEVTLNNTIY-KNDNLVLAFLNKRDTDFHHPHACLKONGAYRCTGYKES 172
 Db 119 KEEDPIHLRCHSWKNTALHKVTVLQNGKGRKYFHNSDFHHPHACLKONGAYRCTGYKES 178
 QY 173 CCPVSSNTVKIQOEFTPRPVLRASSFPQISGNPVTLTCTETQLSLERSDVPLEFR 226
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 RESULT 15
 US-08-433-123-5
 ; Sequence 5, Application US/08433123
 ; Patent No. 6444789
 ; GENERAL INFORMATION:
 ; APPLICANT: LUO, Shun
 ; TITLE OF INVENTION: CD16-II VARIANTS

Db 179 -KNVSETVNITITQGLA--VSTISSFSP-PGYQVSF-CLVMVLLFAVDTLGLYF 227
 RESULT 14
 US-08-667-939A-8
 ; Sequence 8, Application US/08667939A
 ; Patent No. 5998166
 ; GENERAL INFORMATION:
 ; APPLICANT: LUO, Shun
 ; TITLE OF INVENTION: CD16-II VARIANTS
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/667,939A
 ; FILING DATE: 24-JUN-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/433,123
 ; FILING DATE: 03-MAY-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROWDY, Roger L.
 ; REGISTRATION NUMBER: 25,618
 ; REFERENCE/DOCKET NUMBER: LUO-2A
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 233 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-667-939A-8
 Query Match 9.3%; Score 292; DB 2; Length 233;
 Best Local Similarity 35.5%; Pred. No. 2.1e-18;
 Matches 83; Conservative 34; Mismatches 99; Indels 18; Gaps 10;
 QY 1 MLLVLLVLPVSGQFARTPRPIIFLOPPVTWTFQGERVTLTKGFRFYSPQ--KTKWY 58
 Db 4 LLLPTALLLVLSAGMRTEDLPKAVVLEPQWYVLEKSDVTLKCG--AYSPEDNSTQWF 61
 QY 59 HRYLGEILRETDPNLT---EVOESGEYRCQAGSPPLSPVHLDFSSASLILOAPLSVF 114
 Db 62 H---NESLISSQASSYFIDAATVNDGSEYRCQNLSTLSDPVQVLEVHIGWLLQAPRWVF 118
 QY 115 -EGDSVVLRCRAKAEVTLNNTIY-KNDNLVLAFLNKRDTDFHHPHACLKONGAYRCTGYKES 172
 Db 119 KEEDPIHLRCHSWKNTALHKVTVLQNGKGRKYFHNSDFHHPHACLKONGAYRCTGYKES 178
 QY 173 CCPVSSNTVKIQOEFTPRPVLRASSFPQISGNPVTLTCTETQLSLERSDVPLEFR 226
 Db 179 -KNVSETVNITITQGLA--VSTISSFSP-PGYQVSF-CLVMVLLFAVDTLGLYF 227
 RESULT 15
 US-08-433-123-5
 ; Sequence 5, Application US/08433123
 ; Patent No. 6444789
 ; GENERAL INFORMATION:
 ; APPLICANT: LUO, Shun
 ; TITLE OF INVENTION: CD16-II VARIANTS

Search completed: May 4, 2005, 11:55:27
Job time : 20.8351 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:38:21 ; Search time 62.811 Seconds
(without alignments)
3139.559 Million cell updates/sec

Title: US-09-724-254A-3
Perfect score: 3124
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3111	99.6	592	14	US-10-040-862-10461 Sequence 10461, A
2	3111	99.6	592	15	US-10-057-4758-10461 Sequence 10461, A
3	3111	99.6	592	15	US-10-154-8848-10461 Sequence 10461, A
4	3111	99.6	592	15	US-10-403-847-8 Sequence 8, Appli
5	3111	99.6	592	16	US-10-764-324-10461 Sequence 10461, A
6	2950	94.4	759	14	US-10-040-862-10460 Sequence 10460, A
7	2950	94.4	759	15	US-10-057-4758-10460 Sequence 10460, A
8	2950	94.4	759	15	US-10-154-8848-10460 Sequence 10460, A
9	2950	94.4	759	15	US-10-403-847-7 Sequence 7, Appli
10	2950	94.4	759	16	US-10-764-324-10460 Sequence 10460, A
11	2950	94.4	977	14	US-10-040-862-10462 Sequence 10462, A
12	2950	94.4	977	14	US-10-241-220-97 Sequence 97, Appl
13	2950	94.4	977	15	US-10-057-4758-10462 Sequence 10462, A

14	2950	94.4	977	15	US-10-154-8848-10462 Sequence 10462, A
15	2950	94.4	977	15	US-10-403-847-9 Sequence 9, Appli
16	2950	94.4	977	16	US-10-764-324-10462 Sequence 10462, A
17	2924.5	93.6	790	15	US-10-403-847-4 Sequence 4, Appli
18	1854	59.3	438	15	US-10-403-847-6 Sequence 6, Appli
19	1502	48.1	317	15	US-10-403-847-2 Sequence 2, Appli
20	1193.5	38.2	582	15	US-10-162-335-94 Sequence 94, Appl
21	1193.5	38.2	707	15	US-10-108-260A-4774 Sequence 4774, Ap
22	1193.5	38.2	734	14	US-10-040-862-10463 Sequence 10463, A
23	1193.5	38.2	734	15	US-10-057-4758-10463 Sequence 10463, A
24	1193.5	38.2	734	15	US-10-154-8848-10463 Sequence 10463, A
25	1193.5	38.2	734	16	US-10-764-324-10463 Sequence 10463, A
26	1193.5	38.2	734	17	US-10-948-518-137 Sequence 137, App
27	1176	37.6	727	17	US-10-473-519-20 Sequence 20, Appl
28	900	28.8	181	16	US-10-363-829-286 Sequence 286, App
29	900	28.8	181	16	US-10-363-829-431 Sequence 431, App
30	847.5	27.1	639	16	US-10-408-765A-2410 Sequence 2410, Ap
31	826.5	26.5	515	14	US-10-040-862-10459 Sequence 10459, A
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33	826.5	26.5	515	15	US-10-154-8848-10459 Sequence 10459, A
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35	803.5	25.7	421	15	US-10-162-335-96 Sequence 96, Appl
36	803.5	25.7	421	15	US-10-162-335-98 Sequence 98, Appl
37	791	25.3	152	15	US-10-403-847-10 Sequence 10, Appl
38	786.5	25.2	421	15	US-10-162-335-100 Sequence 100, App
39	783.5	25.1	445	15	US-10-154-8848-11043 Sequence 11043, A
40	773.5	24.8	508	14	US-10-040-862-10464 Sequence 10464, A
41	773.5	24.8	508	15	US-10-057-4758-10464 Sequence 10464, A
42	773.5	24.8	508	15	US-10-154-8848-10464 Sequence 10464, A
43	773.5	24.8	508	15	US-10-154-8848-11039 Sequence 11039, A
44	773.5	24.8	508	16	US-10-764-324-10464 Sequence 10464, A
45	773.5	24.8	508	17	US-10-948-518-119 Sequence 119, App

ALIGNMENTS

RESULT 1

US-10-040-862-10461
; Sequence 10461, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416


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Db 541 CTADNGFGPQSEVSVSLFVTGKCWLASHPPLABFSLTHSPKSLFALSSEFLP 592

RESULT 3
US-10-154-884B-10461
; Sequence 10461, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10154, 884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR FILING DATE: 2000-03-01
; PRIOR FILING DATE: 2000-03-01
; PRIOR FILING DATE: 2000-03-17
; PRIOR FILING DATE: 2000-04-27
; PRIOR FILING DATE: 2000-04-28
; PRIOR FILING DATE: 2000-04-28
; PRIOR FILING DATE: 2000-05-01
; PRIOR FILING DATE: 2000-05-01
; PRIOR FILING DATE: 2000-05-04
; PRIOR FILING DATE: 2000-05-22
; PRIOR FILING DATE: 2000-07-14
; PRIOR FILING DATE: 2000-07-14
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10461
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-10461

Qy 1 MLLWVILLVAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTKGFRFYSPOKTKWYHR 60
Db 1 MLLWVILLVAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTKGFRFYSPOKTKWYHR 60

Qy 61 YLGEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQDSV 120
Db 61 YLGEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQDSV 120

Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHPHACLKNDGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHPHACLKNDGAYRCTGYKESCCPVSSNT 180

Qy 181 VKIQVQEPFTRPVLRASSFPISGNPVTLCETQLSLERSDVPLRFRFRDDOTLGLGWS 240
Db 181 VKIQVQEPFTRPVLRASSFPISGNPVTLCETQLSLERSDVPLRFRFRDDOTLGLGWS 240

Qy 241 LSPNFQITAMWSKDSGFYCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
Db 241 LSPNFQITAMWSKDSGFYCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300

Qy 301 GTKVTLLHCEQEDSLRTLRYFYHEGVPLRHKSVRCERGASISFSLTTTENSNGNYCTADNG 360
Db 301 GTKVTLLHCEQEDSLRTLRYFYHEGVPLRHKSVRCERGASISFSLTTTENSNGNYCTADNG 360
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Qy 301 GTKVTLLHCEQEDSLRTLRYFYHEGVPLRHKSVRCERGASISFSLTTTENSNGNYCTADNG 360
Db 301 GTKVTLLHCEQEDSLRTLRYFYHEGVPLRHKSVRCERGASISFSLTTTENSNGNYCTADNG 360

Qy 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHHDDAA 420
Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHHDDAA 420

Qy 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQSKAVSLSIITVPVSHPVLTLSA 480
Db 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQSKAVSLSIITVPVSHPVLTLSA 480

Qy 481 EALTPEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSPFSLTEGHSNYY 540
Db 481 EALTPEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSPFSLTEGHSNYY 540

Qy 541 CTADNGFGPQSEVSVSLFVTGKCWLASKPPLAELFSLTHSPKSLFALSSEFLP 592
Db 541 CTADNGFGPQSEVSVSLFVTGKCWLASHPPLABFSLTHSPKSLFALSSEFLP 592

RESULT 4
US-10-403-847-8
; Sequence 8, Application US/10403847
; Publication No. US20040030098A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLICING VARIANTS OF A HUMAN
; FILE REFERENCE: D0228 NP
; CURRENT APPLICATION NUMBER: US/10/403, 847
; CURRENT FILING DATE: 2003-03-28
; PRIOR FILING DATE: U.S. 60/368, 671
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: U.S. 60/371, 420
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 8
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-847-8

Query Match 99.6%; Score 3111; DB 15; Length 592;
Best Local Similarity 99.7%; Pred. No. 5.8e-235;
Matches 590; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MLLWVILLVAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTKGFRFYSPOKTKWYHR 60
Db 1 MLLWVILLVAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTKGFRFYSPOKTKWYHR 60

Qy 61 YLGEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQDSV 120
Db 61 YLGEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQDSV 120

Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHPHACLKNDGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHPHACLKNDGAYRCTGYKESCCPVSSNT 180

Qy 181 VKIQVQEPFTRPVLRASSFPISGNPVTLCETQLSLERSDVPLRFRFRDDOTLGLGWS 240
Db 181 VKIQVQEPFTRPVLRASSFPISGNPVTLCETQLSLERSDVPLRFRFRDDOTLGLGWS 240

Qy 241 LSPNFQITAMWSKDSGFYCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
Db 241 LSPNFQITAMWSKDSGFYCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300

Qy 301 GTKVTLLHCEQEDSLRTLRYFYHEGVPLRHKSVRCERGASISFSLTTTENSNGNYCTADNG 360
Db 301 GTKVTLLHCEQEDSLRTLRYFYHEGVPLRHKSVRCERGASISFSLTTTENSNGNYCTADNG 360

Qy 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHHDDAA 420
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Db	361	LGAKPSKAVSLSVTVVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA	420
Qy	421	LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTVVSHPVNLSSA	480
Db	421	LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTVVSHPVNLSSA	480
Qy	481	EALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPSVGRVSPFSFSLTEGHSNYY	540
Db	481	EALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPSVGRVSPFSFSLTEGHSNYY	540
Qy	541	CTADNGFGPQRSEVSVLFTVGKWCWLASKPPLAEFSLTHSPKLNLFALSSFLP	592
Db	541	CTADNGFGPQRSEVSVLFTVGKWCWLASHPPPLAEFSLTHSPKLNLFALSSFLP	592
RESULT 5			
US-10-764-324-10461			
; Sequence 10461, Application US/10764324			
; Publication No. US20040175739A1			
; GENERAL INFORMATION:			
; APPLICANT: Gaiger, Alexander			
; APPLICANT: Algate, Paul A.			
; APPLICANT: Mannion, Jane			
; APPLICANT: Retter, Marc			
; APPLICANT: Corixa Corporation			
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy			
; TITLE OF INVENTION: Hematological Malignancies			
; FILE REFERENCE: 014058-013520US			
; CURRENT APPLICATION NUMBER: US/10/764,324			
; CURRENT FILING DATE: 2004-01-23			
; PRIOR APPLICATION NUMBER: US/10/040,862			
; PRIOR FILING DATE: 2001-11-06			
; PRIOR APPLICATION NUMBER: US 60/186,126			
; PRIOR FILING DATE: 2000-03-01			
; PRIOR APPLICATION NUMBER: US 60/190,479			
; PRIOR FILING DATE: 2000-04-27			
; PRIOR APPLICATION NUMBER: US 60/200,303			
; PRIOR FILING DATE: 2000-04-28			
; PRIOR APPLICATION NUMBER: US 60/200,779			
; PRIOR FILING DATE: 2000-05-01			
; PRIOR APPLICATION NUMBER: US 60/202,084			
; PRIOR FILING DATE: 2000-05-04			
; PRIOR APPLICATION NUMBER: US 60/200,545			
; PRIOR FILING DATE: 2000-05-04			
; PRIOR APPLICATION NUMBER: US 60/206,201			
; PRIOR FILING DATE: 2000-05-22			
; PRIOR APPLICATION NUMBER: US 60/218,950			
; PRIOR FILING DATE: 2000-07-14			
; PRIOR APPLICATION NUMBER: US 60/222,903			
; PRIOR FILING DATE: 2000-08-03			
; PRIOR APPLICATION NUMBER: US 60/223,416			
; PRIOR FILING DATE: 2000-08-04			
; PRIOR APPLICATION NUMBER: US 60/223,378			
; PRIOR FILING DATE: 2000-08-07			
; PRIOR APPLICATION NUMBER: US 09/796,692			
; PRIOR FILING DATE: 2001-03-01			
; Query Match 99.6%; Score 3111; DB 16; Length 592;			
; Best Local Similarity 99.7%; Pred. No. 5.8e-235;			
; Matches 590; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
Qy	1	MLLVILLVLPVSGQFARTPRPIIFLQPPWTVFQGERVTLCKGFRFYSPOKTKWYHR	60
Db	1	MLLVILLVLPVSGQFARTPRPIIFLQPPWTVFQGERVTLCKGFRFYSPOKTKWYHR	60
Qy	61	YLGKEILRETPDNILEVQESGEYRCQAGSPVHLDFSSASLIILQAPLSVFEQDSVV	120
Db	61	YLGKEILRETPDNILEVQESGEYRCQAGSPVHLDFSSASLIILQAPLSVFEQDSVV	120
Qy	121	LRCRAKAEVTLNNTIYKNDNVLAFLNKRDPHIFACLKONGAYRCTGYKESCCPVSSNT	180

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; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-10460

Query Match          94.4%; Score 2950; DB 14; Length 759;
Best Local Similarity 98.4%; Pred. No. 3.3e-222;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

Qy 1 MLLWVILLVAPVSGOGFARTPRPIIFLOPPWTVFQGERVTLTKGPRFYSPOKTKWYHR 60
Db 1 MLLWVILLVAPVSGOGFARTPRPIIFLOPPWTVFQGERVTLTKGPRFYSPOKTKWYHR 60
Qy 61 YLKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQSVV 120
Db 61 YLKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEQSVV 120
Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFHACLDKNGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFHACLDKNGAYRCTGYKESCCPVSSNT 180
Qy 181 VKIQVQBPFTPRVLRASSFQIPISGNPVTLCETQLSLERSDVPVLRFRFRDDOTLGLGWS 240
Db 181 VKIQVQBPFTPRVLRASSFQIPISGNPVTLCETQLSLERSDVPVLRFRFRDDOTLGLGWS 240
Qy 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKALNFE 300
Db 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKALNFE 300
Qy 301 GTKVTLHCETQEDSLRTRYFYHGVPLRHKSVCRCERGASISFSLTTENSNGNYCTADNG 360
Db 301 GTKVTLHCETQEDSLRTRYFYHGVPLRHKSVCRCERGASISFSLTTENSNGNYCTADNG 360
Qy 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Db 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Qy 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTVPVSHPVTLSSA 480
Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTVPVSHPVTLSSA 480
Qy 481 EALTFFEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGYY 540
Db 481 EALTFFEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGYY 540
Qy 541 CTADNGFGPQRSEVWSLFTVTKCWVLASKPPL 572
Db 541 CTADNGFGPQRSEVWSLFTVTKCWVLASKPPL 572

RESULT 7
US-10-057-475B-10460
; Sequence 10460, Application US/10057475B
; Publication No. US2004002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
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RESULT 8
US-10-154-884B-10460
; Sequence 10460, Application US/10154884B.
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-10460

Query Match 94.4%; Score 2950; DB 15; Length 759;
Best Local Similarity 98.4%; Pred. No. 3.3e-22;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;
QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRFYSPQTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRFYSPQTKWYHR 60
QY 61 YLCKEILRETPDNILEVQESGEYRCQAQSPVHLDFFSSASLILQAPLSVFEQDSV 120
DB 61 YLCKEILRETPDNILEVQESGEYRCQAQSPVHLDFFSSASLILQAPLSVFEQDSV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDPHIFACLDKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDPHIFACLDKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVEPFRPVLRASSFOPIISGNPVTLCETQLSLERSDVLPRFRFRDDQTLGLWS 240
DB 181 VKIQVEPFRPVLRASSFOPIISGNPVTLCETQLSLERSDVLPRFRFRDDQTLGLWS 240
QY 241 LSPNFQITAMWSKDSGFYWCKAATMPSHVISDSPRSNIQVQIPASHPVLTLSPKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYWCKAATMPSHVISDSPRSNIQVQIPASHPVLTLSPKALNFE 300
QY 301 GTKVTLHCETQDSRLTYRFYHEGVPLRHKSVCRCERGASISFSLTENSNGNYCTADNG 360
DB 301 GTKVTLHCETQDSRLTYRFYHEGVPLRHKSVCRCERGASISFSLTENSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEKAKVTLHCEAQRGSLPILYQFHEDAA 420

Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEKAKVTLHCEAQRGSLPILYQFHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYCYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
Db 421 LERRSANSAGGVAISFSLTAHSGNYCYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
QY 481 EALTFEAGATVTLHCEVORGSPQIILYQFYHEDMPLVSSSTPSVGRVSFSLTEHSGNYY 540
Db 481 EALTFEAGATVTLHCEVORGSPQIILYQFYHEDMPLVSSSTPSVGRVSFSLTEHSGNYY 540
QY 541 CTADNGFGPQRSSEVVSFLVTKCWVLASKPPL 572
Db 541 CTADNGFGPQRSSEVVSFLVTKCWVLASKPPL 572
RESULT 9
US-10-403-847-7
; Sequence 7, Application US/10403847
; Publication No. US20040030098A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLIC VARIANTS OF A HUMAN
; TITLE OF INVENTION: CELL SURFACE PROTEIN WITH IMMUNOLOGOBULIN FOLDS, BGS5G AND BGS5I
; FILE REFERENCE: D0228 NP
; CURRENT APPLICATION NUMBER: US/10/403,847
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: U.S. 60/368,671
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: U.S. 60/371,420
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-847-7

Query Match 94.4%; Score 2950; DB 15; Length 759;
Best Local Similarity 98.4%; Pred. No. 3.3e-22;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;
QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRFYSPQTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRFYSPQTKWYHR 60
QY 61 YLCKEILRETPDNILEVQESGEYRCQAQSPVHLDFFSSASLILQAPLSVFEQDSV 120
DB 61 YLCKEILRETPDNILEVQESGEYRCQAQSPVHLDFFSSASLILQAPLSVFEQDSV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDPHIFACLDKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDPHIFACLDKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVEPFRPVLRASSFOPIISGNPVTLCETQLSLERSDVLPRFRFRDDQTLGLWS 240
DB 181 VKIQVEPFRPVLRASSFOPIISGNPVTLCETQLSLERSDVLPRFRFRDDQTLGLWS 240
QY 241 LSPNFQITAMWSKDSGFYWCKAATMPSHVISDSPRSNIQVQIPASHPVLTLSPKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYWCKAATMPSHVISDSPRSNIQVQIPASHPVLTLSPKALNFE 300
QY 301 GTKVTLHCETQDSRLTYRFYHEGVPLRHKSVCRCERGASISFSLTENSNGNYCTADNG 360
DB 301 GTKVTLHCETQDSRLTYRFYHEGVPLRHKSVCRCERGASISFSLTENSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEKAKVTLHCEAQRGSLPILYQFHEDAA 420
Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEKAKVTLHCEAQRGSLPILYQFHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYCYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480

Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
Qy 481 EALTPEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGNY 540
Db 481 EALTPEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGNY 540
Qy 541 CTADNGFGPQRSEVSVLFTVKCKWLASKPPL 572
Db 541 CTADNGFGPQRSEVSVLFTVKCKWLASKPPL 568

RESULT 10
US-10-764-324-10460
; Sequence 10460, Application US/10764324
; Publication No. US2004017539A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/764,324
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR FILING DATE: 2000-03-01
; PRIOR FILING DATE: 2000-03-17
; PRIOR FILING DATE: 2000-04-27
; PRIOR FILING DATE: 2000-04-28
; PRIOR FILING DATE: 2000-04-28
; PRIOR FILING DATE: 2000-04-28
; PRIOR FILING DATE: 2000-05-01
; PRIOR FILING DATE: 2000-05-04
; PRIOR FILING DATE: 2000-05-22
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-324-10460

Query Match 94.4%; Score 2950; DB 16; Length 759;
Best Local Similarity 98.4%; Pred. No. 3.3e-222;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

Qy 1 MLLWVILLVLPVSGQFARTPRPIIFLOPWTTFQGERVTLCKGFRFYSPQTKWYHR 60
Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOPWTTFQGERVTLCKGFRFYSPQTKWYHR 60
Qy 61 YLGEILRETPDNLVEQESGEYRCQAGSPVHLDFSSASLILOAPLSVFEQSVV 120
Db 61 YLGEILRETPDNLVEQESGEYRCQAGSPVHLDFSSASLILOAPLSVFEQSVV 120
Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFHACLKONGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFHACLKONGAYRCTGYKESCCPVSSNT 180
Qy 181 VKIQVQEPFTRPVLRASSFQIPISGNPVTLTCETOLSLERSDVPVLRFRFRDDQTLGLGWS 240

Db 181 VKIQVQEPFTRPVLRASSFQIPISGNPVTLTCETOLSLERSDVPVLRFRFRDDQTLGLGWS 240
Qy 241 LSPNFQITAMWSKDSGFYWCXKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
Db 241 LSPNFQITAMWSKDSGFYWCXKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
Qy 301 GTKVTLHCETQEDSLRTLRYFYHGVPLRHKSVCRCGASISFSLTTENSNGNYCTADNG 360
Db 301 GTKVTLHCETQEDSLRTLRYFYHGVPLRHKSVCRCGASISFSLTTENSNGNYCTADNG 360
Qy 361 LGAKPSKAVSLSVTPVSHPVLTLSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Db 361 LGAKPSKAVSLSVTPVSHPVLTLSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Qy 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
Qy 481 EALTPEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGNY 540
Db 481 EALTPEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGNY 540
Qy 541 CTADNGFGPQRSEVSVLFTVKCKWLASKPPL 572
Db 541 CTADNGFGPQRSEVSVLFTVKCKWLASKPPL 568

RESULT 11
US-10-040-862-10462
; Sequence 10462, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10462
; LENGTH: 977
; TYPE: PRT

Query Match 94.4%; Score 2950; DB 14; Length 977;
Best Local Similarity 98.4%; Pred. No. 4.7e-222;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

1 MLLWVILLVAPVSGOFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSPOKTKWYHR 60
1 MLLWVILLVAPVSGOFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSPOKTKWYHR 60

61 YLKEILRETPDNILEVOESGYSRCAQSPVHLDFSSASLILQAPLSVFEKGSVV 120
61 YLKEILRETPDNILEVOESGYSRCAQSPVHLDFSSASLILQAPLSVFEKGSVV 120

121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180
121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180

181 VKIQVQEPFTRPVLRASSFPISGNPVTLTCTQLSLERSDVPLRFRFRDDQTLGLGWS 240
181 VKIQVQEPFTRPVLRASSFPISGNPVTLTCTQLSLERSDVPLRFRFRDDQTLGLGWS 240

241 LSPNFOITAMWSKDSGFYCKAATMPSHVSIDSPRSWIOVQIPASHVPLTLSPEKALNFE 300
241 LSPNFOITAMWSKDSGFYCKAATMPSHVSIDSPRSWIOVQIPASHVPLTLSPEKALNFE 300

301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTTTENSNGNYCTADNG 360
301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTTTENSNGNYCTADNG 360

361 LGAKPSKAVSLSVTPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRSLPILYQFHEDAA 420
361 LGAKPSKAVSLSVTPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRSLPILYQFHEDAA 420

421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSIITVPVSHVPLTLSA 480
421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSIITVPVSHVPLTLSA 480

481 EALTPEGATVTLHCEVQRSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGNY 540
481 EALTPEGATVTLHCEVQRSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGNY 540

541 CTADNGFGPQRSEVSVLFTGCKWVLASKPPL 572
541 CTADNGFGPQRSEVSVLFTGCKWVLASKPPL 572

RESULT 13
US-10-057-475B-10462
; Sequence 10462, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779

Query Match 94.4%; Score 2950; DB 14; Length 977;
Best Local Similarity 98.4%; Pred. No. 4.7e-222;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

1 MLLWVILLVAPVSGOFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSPOKTKWYHR 60
1 MLLWVILLVAPVSGOFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSPOKTKWYHR 60

61 YLKEILRETPDNILEVOESGYSRCAQSPVHLDFSSASLILQAPLSVFEKGSVV 120
61 YLKEILRETPDNILEVOESGYSRCAQSPVHLDFSSASLILQAPLSVFEKGSVV 120

121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180
121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180

181 VKIQVQEPFTRPVLRASSFPISGNPVTLTCTQLSLERSDVPLRFRFRDDQTLGLGWS 240
181 VKIQVQEPFTRPVLRASSFPISGNPVTLTCTQLSLERSDVPLRFRFRDDQTLGLGWS 240

241 LSPNFOITAMWSKDSGFYCKAATMPSHVSIDSPRSWIOVQIPASHVPLTLSPEKALNFE 300
241 LSPNFOITAMWSKDSGFYCKAATMPSHVSIDSPRSWIOVQIPASHVPLTLSPEKALNFE 300

301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTTTENSNGNYCTADNG 360
301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTTTENSNGNYCTADNG 360

361 LGAKPSKAVSLSVTPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRSLPILYQFHEDAA 420
361 LGAKPSKAVSLSVTPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRSLPILYQFHEDAA 420

421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSIITVPVSHVPLTLSA 480
421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSIITVPVSHVPLTLSA 480

481 EALTPEGATVTLHCEVQRSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGNY 540
481 EALTPEGATVTLHCEVQRSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGNY 540

541 CTADNGFGPQRSEVSVLFTGCKWVLASKPPL 572
541 CTADNGFGPQRSEVSVLFTGCKWVLASKPPL 572

RESULT 12
US-10-241-220-97
; Sequence 97, Application US/10241220
; Publication No. US20030148408A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/241,220
; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 97
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-241-220-97

; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10462
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-10462

Query Match 94.4%; Score 2950; DB 15; Length 977;
Best Local Similarity 98.4%; Pred. No. 4.7e-222;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

QY 1 MLLWVILLVLPVSGQPARTPRPIIFLOPPWTTVFOGERTVLTCKGPRFYSPOKTKWYHR 60
DB 1 MLLWVILLVLPVSGQPARTPRPIIFLOPPWTTVFOGERTVLTCKGPRFYSPOKTKWYHR 60
QY 61 YLGEILRETPDNILVQESGEYRCQAQGSPLSPVHLDFSSASLILQAPLSVFEQGSVV 120
DB 61 YLGEILRETPDNILVQESGEYRCQAQGSPLSPVHLDFSSASLILQAPLSVFEQGSVV 120
QY 121 LRCRAKAEVTNNIYKNDNVLAFLNKRDTDFHIFHACLKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTNNIYKNDNVLAFLNKRDTDFHIFHACLKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVEPFRPVLRASSQPIISGNPVTLCETQLSLERSDVLPRFRFRDDOTLGLGWS 240
DB 181 VKIQVEPFRPVLRASSQPIISGNPVTLCETQLSLERSDVLPRFRFRDDOTLGLGWS 240
QY 241 LSPNFQITAMWSKDSGYWCKAATMPHSVSDSPRSWIOVOIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFQITAMWSKDSGYWCKAATMPHSVSDSPRSWIOVOIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTENSNGNYCTADNG 360
DB 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTENSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
QY 481 EALTFFEGATVTLHCEVQSGPQLLYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSGNYY 540
DB 481 EALTFFEGATVTLHCEVQSGPQLLYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSGNYY 540
QY 541 CTADNGFGPORSVWSLFTVTKGCWVLAKPPL 572
DB 541 CTADNGFGPORSVWSLFTVTKGCWVLAKPPL 572

RESULT 14
US-10-154-884B-10462
; Sequence 10462, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane

; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10462
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-10462

Query Match 94.4%; Score 2950; DB 15; Length 977;
Best Local Similarity 98.4%; Pred. No. 4.7e-222;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

QY 1 MLLWVILLVLPVSGQPARTPRPIIFLOPPWTTVFOGERTVLTCKGPRFYSPOKTKWYHR 60
DB 1 MLLWVILLVLPVSGQPARTPRPIIFLOPPWTTVFOGERTVLTCKGPRFYSPOKTKWYHR 60
QY 61 YLGEILRETPDNILVQESGEYRCQAQGSPLSPVHLDFSSASLILQAPLSVFEQGSVV 120
DB 61 YLGEILRETPDNILVQESGEYRCQAQGSPLSPVHLDFSSASLILQAPLSVFEQGSVV 120
QY 121 LRCRAKAEVTNNIYKNDNVLAFLNKRDTDFHIFHACLKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTNNIYKNDNVLAFLNKRDTDFHIFHACLKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVEPFRPVLRASSQPIISGNPVTLCETQLSLERSDVLPRFRFRDDOTLGLGWS 240
DB 181 VKIQVEPFRPVLRASSQPIISGNPVTLCETQLSLERSDVLPRFRFRDDOTLGLGWS 240
QY 241 LSPNFQITAMWSKDSGYWCKAATMPHSVSDSPRSWIOVOIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFQITAMWSKDSGYWCKAATMPHSVSDSPRSWIOVOIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTENSNGNYCTADNG 360
DB 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTENSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
QY 481 EALTFFEGATVTLHCEVQSGPQLLYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSGNYY 540

Db 541 CTADNGFGPQSEVWSLFVT----VPVSRPIL 568

Search completed: May 4, 2005, 12:01:15
Job time : 64.811 secs

Db 481 EALTTEGATVTLHCEVQSGSQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGYY 540
QY 541 CTADNGFGPQSEVWSLFVTGKCWLASKPPL 572
Db 541 CTADNGFGPQSEVWSLFVT----VPVSRPIL 568

RESULT 15
US-10-403-847-9
; Sequence 9, Application US/10403847
; Publication NO. US20040030098A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLICE VARIANTS OF A HUMAN
; TITLE OF INVENTION: CELL SURFACE PROTEIN WITH IMMUNOGLOBULIN FOLDS, BGS5G AND BGS5I
; FILE REFERENCE: D0228 NP
; CURRENT APPLICATION NUMBER: US/10/403,847
; CURRENT FILING DATE: 2003-03-28
; PRIOR FILING DATE: U.S. 60/368,671
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: U.S. 60/371,420
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-847-9

Query Match 94.4%; Score 2950; DB 15; Length 977;
Best Local Similarity 98.4%; Pred. No. 4.7e-222;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPWTTVFQGERVTLTCKGFRFYSQKTKWYHR 60
Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOPWTTVFQGERVTLTCKGFRFYSQKTKWYHR 60
QY 61 YLGEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDPSSASLILOAPLSVFEGDSVV 120
Db 61 YLGEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDPSSASLILOAPLSVFEGDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDVLAFLNKRTDFHPHACLKNDGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDVLAFLNKRTDFHPHACLKNDGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQPPFTRPVLRASSFQIPISGNPVTLCETQLSLERSDVLPRFRFRDDQTLGLGWS 240
Db 181 VKIQVQPPFTRPVLRASSFQIPISGNPVTLCETQLSLERSDVLPRFRFRDDQTLGLGWS 240
QY 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVISDSRSHIQVQIPASHPVLTLSPKALNFE 300
Db 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVISDSRSHIQVQIPASHPVLTLSPKALNFE 300
QY 301 GTKVTLHCETQEDSLRTLRYRHYEGVPLRHKSVRCERGASISFSLTTENSNGNYCTADNG 360
Db 301 GTKVTLHCETQEDSLRTLRYRHYEGVPLRHKSVRCERGASISFSLTTENSNGNYCTADNG 360
QY 361 LGAKPSKAVLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQGSLPILYQPHHEDAA 420
Db 361 LGAKPSKAVLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQGSLPILYQPHHEDAA 420
QY 421 LERRANSAGGVAISFSLTAHSGNYCTADNGFGPQSKAVLSITVPVSHPVLTLSA 480
Db 421 LERRANSAGGVAISFSLTAHSGNYCTADNGFGPQSKAVLSITVPVSHPVLTLSA 480
QY 481 EALTTEGATVTLHCEVQSGSQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGYY 540
Db 481 EALTTEGATVTLHCEVQSGSQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGYY 540
QY 541 CTADNGFGPQSEVWSLFVTGKCWLASKPPL 572

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:24:30 ; Search time 18.5636 Seconds
(without alignments)
3068.392 Million cell updates/sec

Title: US-09-724-254A-3
Perfect score: 3124
Sequence: 1 MLWVILLVLPVSGQFART.....AEPSLTHSFKNLPSLSFLP 592

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	418.5	13.4	344	2 A41357	Fc gamma (IgG) rec
2	418.5	13.4	374	1 A39878	Fc gamma (IgG) rec
3	402.5	12.9	404	2 A46480	Fc gamma (IgG) rec
4	396	12.7	336	2 I48471	Fc gamma (IgG) rec
5	326.5	10.5	296	2 I46021	Fc-gamma receptor
6	319	10.2	270	2 A34636	Fc-gamma receptor
7	299.5	9.6	4391	2 A38096	perlecan precursor
8	292.5	9.4	254	1 JL0107	Fc gamma (IgG) rec
9	292	9.3	233	1 JU0284	Fc gamma (IgG) rec
10	290	9.3	323	2 S06946	Fc gamma (IgG) rec
11	289	9.3	310	2 JL0119	Fc gamma (IgG) rec
12	275	8.8	7962	2 I38436	elastic titin - hu
13	272	8.7	255	2 JC7593	SH2 domain-contain
14	267	8.5	257	2 S00682	IgE Fc receptor al
15	264.5	8.5	317	2 JL0118	Fc gamma (IgG) rec
16	262	8.4	285	2 S36903	Fc gamma (IgG) rec
17	258	8.3	3707	2 S18252	heparan sulfate pr
18	257	8.2	261	2 S29360	Fc gamma (IgG) rec
19	256	8.2	280	2 I55577	Fc gamma (IgG) rec
20	253.5	8.1	283	1 FCMG51	Fc gamma (IgG) rec
21	253.5	8.1	330	2 A40071	Fc gamma (IgG) rec
22	253.5	8.1	330	2 I49660	Fc-gamma-1/gamma-2
23	248.5	8.1	1256	2 T03096	CDO protein - rat
24	248.5	8.0	738	2 A40096	platelet-endotheli
25	244	7.8	267	2 I56110	Fc-gamma RIIB- α p
26	241	7.7	1694	2 S00655	sialoadhesin - mou
27	241	7.7	1896	2 T08851	Down syndrome cell
28	240	7.7	862	2 I49583	differentiation an
29	235.5	7.5	1240	2 T03097	CDO protein - huma

CD22 homolog/B lym
carcinoembryonic a
BIG-1 protein - ra
Fc gamma (IgG) rec
B-cell adhesion pr
immunoglobulin-lik
axonal glycoprotei
IgE receptor alpha
connectin 3B - chi
connectin/titin -
axonin 1 precursor
hypothetical prote
hemictenin precurs
cell adhesion prot
hypothetical prote
plasmacytoma-assoc

ALIGNMENTS

RESULT 1

A41357
Fc gamma (IgG) receptor 1 (high affinity) form b - human
N;Alternate names: CD64
C;Species: Homo sapiens (man)
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004
C;Accession: A41357; S03019
R;Allen, J.M.; Seed, B.
Science 243, 378-381, 1989
A;Title: Isolation and expression of functional high-affinity Fc receptor complementary I
A;Reference number: A41357; MUID:89100284; PMID:2911749
A;Accession: A41357
A;Molecule type: mRNA
A;Residues: 1-344 <ALL>
A;Cross-references: UNIPROT:P12314; GB:X14355; GB:M21090; NID:G31333; PIDN:CAA32536.1; P
R;Allen, J.M.; Seed, B.
Nucleic Acids Res. 16, 11824, 1988
A;Title: Nucleotide sequence of three cDNAs for the human high affinity Fc receptor (FcR
A;Reference number: S03018; MUID:89098339; PMID:2974947
A;Accession: S03019
A;Molecule type: mRNA
A;Residues: 1-344 <ALL>
A;Cross-references: EMBL:X14355; NID:G31333; PIDN:CAA32536.1; PID:G31334
A;Note: the authors translated the codon ACT for residue 25 as Ala
C;Superfamily: Fc gamma receptor I; immunoglobulin homology
C;Keywords: alternative splicing; immunoglobulin receptor; transmembrane protein
F;117-170/Domain: immunoglobulin homology <IMM>

Query Match		13.4%	Score 418.5;	DB 2;	Length 344;
Best Local Similarity		37.0%	Pred. No. 8.2e-21;		
Matches 108;		Conservative 41;	Mismatches 122;	Indels 21;	Gaps 10;
QY	1	MLWVILLVLPVSGQFARTPRPIIFLOPPTWTVFGQGVTLTKGKFRFRFSPQTKVYHR	60		
DB	7	LLWV-----PVDGG-VDTTKAVITLOPPWVSVFQETVTLHCEVHLHLPSSSTOMFLN	59		
QY	61	YLQKEILRETPD---NILEVOESGEYRCAQGSPLSSPVHLDFFSSASLILOAPLSVF-EG	116		
DB	60	--GTATQTPSPYRITSASVNDSGEYRCQGLSGRSDPTQLEIHRGWLLQVSRVFTG	117		
QY	117	DSVVLRCRA-KAEVTLNNTIYKNDNVLAFLNKRKTDPHIACLKDKNGAYRCTGYKESCCP	175		
DB	118	EPLALACHAWKDKLVNVLVYRNGKAFKFFHWNLSNLTILKTNISHNGTVHSCGNGKH--R	175		
QY	176	VSSNTVKIQVEPFTFPVLRASSFQ-IGSNPVTLTCEQTSLSLERSDVPLRFFRRDDQT	234		
DB	176	YTSAGISVTVKELFPAPVLNASVTSLEEGNLVTLSCETKLLQRPGLQLYFSFYNGSKT	235		
QY	235	LGIQWLSNPFQITAMWMSKDSGFYWCKAATMPHSVSDSPRSMIOV---QIP	283		
DB	236	L-RGRNTSEYQLLTARRSDSGLYWCEAATDGNLKRSPLELQVLGLQLP	286		

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us-09-724-254a-3.rpr

```

60  --GTATQTSTPSYRITSVNDSDGEYRCQGLSGRSDPIQLIHRGMLLLQVSSRVFTG 117
117 DSVVLRCA-KAEVTLNNTIYKNDNVLAFLNKRDTDFHAPHACLKNDNGAYRCTGYKESCCP 175
118 EPLALRCHAWKDKLVYVNVLYRNGKAFKFFHWNLSNLTILKTNISINGYHCSGMGKH--R 175
176 VSSNTVKIQVQBPFRPVLRASSFOF-ISGNPVTITCTQLSLERSDVLPRFRFRDQOT 234
176 YTSAGISVTIKELFPAPVLNASVTSPLLEGLNLTLSCTELKLLQRPGLQVPSFYMGSKT 235
235 LGLGWSLSNPNQITAMWSKDSGFYCKAAATMPSHVISDSPRSWIQV--OIP 283
236 L-RGRNTSSEYQILTARREDSGLYWCCEATEDGNVLRKSPLELQVLGLQLP 286

RESULT 3
A6480
Fc gamma (IgG) receptor high affinity - mouse
N:Alternate names: high affinity IgG receptor
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A46480; A43511
R:Osman, N.; Kozak, C.A.; McKenzie, I.F.; Hogarth, P.M.
J:Immunol. 148, 1570-1575, 1992
A:Title: Structure and mapping of the gene encoding mouse high affinity Fc gamma RI and
A:Reference number: A46480; MUID:92166399; PMID:1531670
A:Accession: A46480
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-404 <OSM>
A:Cross-references: UNIPROT:P26151
A:Note: sequence extracted from NCBI backbone (NCBIN:85205, NCBIN:85208, NCBIN:85212, NCI
R:Sears, D.W.; Osman, N.; Tate, B.; McKenzie, I.F.C.; Hogarth, P.M.
J:Immunol. 144, 371-378, 1990
A:Title: Molecular cloning and expression of the mouse high affinity Fc receptor for IgG
A:Reference number: A43511; MUID:90111035; PMID:2136886
A:Accession: A43511
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-404 <SEA>
A:Cross-references: GB:M31314; NID:g200752; PID:AAA40056.1; PID:g200753
C:Superfamily: Fc gamma receptor I; immunoglobulin homology
C:Keywords: immunoglobulin receptor; transmembrane protein
F:127-179/Domain: immunoglobulin homology <IMW>

Query Match 12.9%; Score 402.5; DB 2; Length 404;
Best Local Similarity 36.3%; Pred. No. 1.2e-19;
Matches 107; Conservative 42; Mismatches 131; Indels 15; Gaps 10;

QY 3 LMVI--LLVLAPVSGQFARTPRPIIFLOPPWTTFVQGERVLTCKGFRFSPQTKWYHR 60
10 MWLLTLLLVPEVGVVNAVTKAVITLQPPWVSIFQXENVTLWCEGPHLPDGSSTQWFN 69
61 YLGKEILRETPDNIL---EVQESGEYRCQAQSPSSPVHLDFFSSASILQAPLSVVF-EG 116
70 --GTAVQISTPSYSIPEASFOQSGEYRCQIGSSMPSPVQLQIHNWLLQASRVLTG 127
117 DSVVLRCA-KAEVTLNNTIYKNDNVLAFLNKRDTDFHAPHACLKNDNGAYRCTGYKESCCP 175
128 EPLALRCHGWKDKLVYVNVLYRNGSKSFQF-SSDSEVALKTNLSHGSIYHCSGTGRH--R 184
176 VSSNTVKIQVQBPFRPVLRASSFOPI-SGNPVTITCTQLSLERSDVLPRFRFRDQOT 234
185 YTSAGISVTIKELFTTFVLRASVSSFPFPGSLVTLNCTENLLQRPGLQVPSFYVSGKI 244
235 LGLGWSLSNPNQITAMWSKDSGFYCKAAATMPSHVISDSPRSWIQVQIP-ASHPV 288
245 LEVR-NTSSEYHIAEREDAGFYWCCEATEDGNVLRKSPLELQVLGLQLP 286

RESULT 4
148471
Fc gamma (IgG) receptor high affinity - mouse

Db 60  --GTATQTSTPSYRITSVNDSDGEYRCQGLSGRSDPIQLIHRGMLLLQVSSRVFTG 117
QY 117 DSVVLRCA-KAEVTLNNTIYKNDNVLAFLNKRDTDFHAPHACLKNDNGAYRCTGYKESCCP 175
Db 118 EPLALRCHAWKDKLVYVNVLYRNGKAFKFFHWNLSNLTILKTNISINGYHCSGMGKH--R 175
QY 176 VSSNTVKIQVQBPFRPVLRASSFOF-ISGNPVTITCTQLSLERSDVLPRFRFRDQOT 234
Db 176 YTSAGISVTIKELFPAPVLNASVTSPLLEGLNLTLSCTELKLLQRPGLQVPSFYMGSKT 235
QY 235 LGLGWSLSNPNQITAMWSKDSGFYCKAAATMPSHVISDSPRSWIQV--OIP 283
Db 236 L-RGRNTSSEYQILTARREDSGLYWCCEATEDGNVLRKSPLELQVLGLQLP 286

RESULT 3
A6480
Fc gamma (IgG) receptor high affinity - mouse
N:Alternate names: high affinity IgG receptor
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A46480; A43511
R:Osman, N.; Kozak, C.A.; McKenzie, I.F.; Hogarth, P.M.
J:Immunol. 148, 1570-1575, 1992
A:Title: Structure and mapping of the gene encoding mouse high affinity Fc gamma RI and
A:Reference number: A46480; MUID:92166399; PMID:1531670
A:Accession: A46480
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-404 <OSM>
A:Cross-references: UNIPROT:P26151
A:Note: sequence extracted from NCBI backbone (NCBIN:85205, NCBIN:85208, NCBIN:85212, NCI
R:Sears, D.W.; Osman, N.; Tate, B.; McKenzie, I.F.C.; Hogarth, P.M.
J:Immunol. 144, 371-378, 1990
A:Title: Molecular cloning and expression of the mouse high affinity Fc receptor for IgG
A:Reference number: A43511; MUID:90111035; PMID:2136886
A:Accession: A43511
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-404 <SEA>
A:Cross-references: GB:M31314; NID:g200752; PID:AAA40056.1; PID:g200753
C:Superfamily: Fc gamma receptor I; immunoglobulin homology
C:Keywords: immunoglobulin receptor; transmembrane protein
F:127-179/Domain: immunoglobulin homology <IMW>

Query Match 12.9%; Score 402.5; DB 2; Length 404;
Best Local Similarity 36.3%; Pred. No. 1.2e-19;
Matches 107; Conservative 42; Mismatches 131; Indels 15; Gaps 10;

QY 3 LMVI--LLVLAPVSGQFARTPRPIIFLOPPWTTFVQGERVLTCKGFRFSPQTKWYHR 60
Db 10 MWLLTLLLVPEVGVVNAVTKAVITLQPPWVSIFQXENVTLWCEGPHLPDGSSTQWFN 69
QY 61 YLGKEILRETPDNIL---EVQESGEYRCQAQSPSSPVHLDFFSSASILQAPLSVVF-EG 116
Db 70 --GTAVQISTPSYSIPEASFOQSGEYRCQIGSSMPSPVQLQIHNWLLQASRVLTG 127
QY 117 DSVVLRCA-KAEVTLNNTIYKNDNVLAFLNKRDTDFHAPHACLKNDNGAYRCTGYKESCCP 175
Db 128 EPLALRCHGWKDKLVYVNVLYRNGSKSFQF-SSDSEVALKTNLSHGSIYHCSGTGRH--R 184
QY 176 VSSNTVKIQVQBPFRPVLRASSFOPI-SGNPVTITCTQLSLERSDVLPRFRFRDQOT 234
Db 185 YTSAGISVTIKELFTTFVLRASVSSFPFPGSLVTLNCTENLLQRPGLQVPSFYVSGKI 244
QY 235 LGLGWSLSNPNQITAMWSKDSGFYCKAAATMPSHVISDSPRSWIQVQIP-ASHPV 288
Db 245 LEVR-NTSSEYHIAEREDAGFYWCCEATEDGNVLRKSPLELQVLGLQLP 286

RESULT 4
148471
Fc gamma (IgG) receptor high affinity - mouse
```

C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C/Accession: I48471
R/Prins, J.B.; Todd, J.A.; Rodrigues, N.R.; Ghosh, S.; Hogarth, P.M.; Wicker, L.S.; Gaff
Science 260, 695-698, 1993
A>Title: Linkage on chromosome 3 of autoimmune diabetes and defective Fc receptor for Ig
A:Reference number: I48471; MUID:93242399; PMID:8480181
A:Accession: I48471
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-336 <RES>
A/Cross-references: EMBL:X70980; NID:g311748; PIDN:CAA50311.1; PID:g311749
C/Superfamily: Fc gamma receptor I; immunoglobulin homology
C/Keywords: immunoglobulin receptor
F:128-180/Domain: immunoglobulin homology <IMM>

Query Match 12.7% Score 396; DB 2; Length 336;
Best Local Similarity 36.1%; Pred. No. 2.6e-19;
Matches 106; Conservative 43; Mismatches 130; Indels 18; Gaps 12;

Qy 3 LWI--LLVLAPVSGQFARTPRIFILOPWTTVFOGERVTLTCKGFRFYSPQKTWYHR 60
 ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::
Db 10 MLWLTTLLWPVGGEVVNATKAVITLQPWSAIFQKENVTLWCGRPHLPDGSSTWFNF 69
 ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::
Qy 61 YLGKEILRETPD---NILEVOEGEVCRAQGSPGLSPVHLDFSSAS-LILOAPLSVF-B 115
 ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::
Db 70 --GTVQTSTPSYSIVASFDGSEYRCQIGSSVPDPVOLQIHKEDWLLQLASRRVLTE 127
 ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::
Qy 116 GDSVVLRCRA-KAEVTLNNTIYNNDNVLAFLNKRTDFHHPACLKONGAYRCTG---YKE 171
 ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::
Db 128 GEPLALCKCHGNKNLVNVVFNKGSFKF-SGSKTIALTKNLSHGISYHCSTMGRHY 186
 ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::
Qy 172 SCCPVSNNTVKIQVEBPFTPLVRASSFQPI-SCNPVTLTCETQLSLERSDVPLRFRRFFR 230
 ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::
Db 187 TSAGVSI-TVKAPELLEFTPLVRASVSFPFGSLVTLNCETNALLQRPGLQLYSFVY 245
 ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::
Qy 231 DDOTLGLGWLSNPFQITAMWSKDGSPYCKAAATMPHSVISDSPRSNIQVIP-AHPV 288
 ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::
Db 246 GSKILEYR-NTSSEYHIARAERDAGPYWCEVATEDSSVLKHSPKLEQLVLGPQSAPV 303
 ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::

RESULT 5

I46021
Fc-gamma receptor II - bovine
C/Species: Bos primigenius taurus (cattle)
C/Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C/Accession: I46021; S4204
R/Zhang, G.; Young, J.R.; Tregaskes, C.R.; Howard, C.J.
Immunogenetics 39, 423-427, 1994
A>Title: Cattle Fc gamma RII: molecular cloning and ligand specificity.
A:Reference number: I46021; MUID:94245284; PMID:8188320
A:Accession: I46021
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-296 <SHA>
A/Cross-references: UNIPROT:Q28110; EMBL:X75671; NID:g437978; PIDN:CAA53367.1; PID:g4379
C/Superfamily: Fc gamma receptor III; immunoglobulin homology
C/Keywords: immunoglobulin receptor

Query Match 10.5% Score 326.5; DB 2; Length 296;
Best Local Similarity 37.0%; Pred. No. 1e-14;
Matches 90; Conservative 34; Mismatches 100; Indels 19; Gaps 10;

Qy 1 MLWLVLVLAPVSGQFARTPRIFILOPWTTVFOGERVTLTCKGFRFYSPQKTWYHR 60
 ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::
Db 28 MLWLTAFLFAPVSGK-PDLPAVVIQPAWINVLREDHVHTLTLCQGFSAAGNLTTFWN 86
 ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::
Qy 61 YLGKEI-LRETDPNILEV--QESGEVCRAQGSPLSPVHLDFSSASLIQAPLSVF-BG 116
 ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::
Db 87 --GSSHTQKQPSYFRAGNSDSSGRCQEQTSLSDPVLHDVISDWLLLTQPSLVFQEG 144
 ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::
Qy 117 DSVVLRCRAKAEVTLNN-TIYNKDNVLAFLNKRTDFHHPACLKONGAYRCTGYKSCCP 175
 ::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::

Query Match	9.6%;	Score 299.5;	DB 2;	Length 4391;
Best Local Similarity	23.5%;	Pred. No. 2.1e-11;	Indels 117;	Gaps 28;
		on. mismatches 264;		

R; Scallan, B.J.; Scigliano, E.; Freedman, V.H.; Miedel, M.C.; Fan, I.C.E.; Smollett, J.S. A 86 5079-5083. 1989

A;Cross-references: UNIPROT:O75015; GB:J04162
A;Note: the sequence of the receptor from human NK cells, reported in the same paper, differs by one amino acid at position 18.
R;Simmons, D.; Seed, B.
Nature 333, 568-570, 1988
A;Title: The Fc-gamma receptor of natural killer cells is a phospholipid-linked membrane protein.
A;Reference number: S00758; MUID:88232937; PMID:2967436
A;Accession: S00758
A;Molecule type: mRNA
A;Residues: 1-233 <STM>
A;Cross-references: EMBL:X07934; NID:g29744; PIDN:CRAA30758.1; PID:g29745
E;Gassner, J.E.; Grusenmeyer, T.; Kolanus, W.; Schmidt, R.E.
J. Biol. Chem. 270, 1350-1361, 1995
A;Title: The human low affinity immunoglobulin G Fc receptor III-A and III-B genes. Molecular cloning and characterization of the cDNA clones.
A;Reference number: A55439; MUID:95138131; PMID:7836402
A;Accession: I37628
A;Molecule type: DNA
A;Residues: 1-72 <RES>
A;Cross-references: EMBL:Z46223; NID:g559446; PIDN:CAA8C296.1; PID:g871306
R;Scallan, B.J.; Scigliano, E.; Freedman, V.H.; Miedel, M.C.; Pan, Y.C.E.; Unkeless, J.C.
Proc. Natl. Acad. Sci. U.S.A. 86, 5079-5083, 1989
A;Title: A human immunoglobulin G receptor exists in both polypeptide-anchored and phospha-
tized forms.
A;Reference number: A32933; MUID:89296947; PMID:2525780
A;Accession: B32933
A;Molecule type: mRNA
A;Residues: 1-121,'E',123-150,'S',152-233 <SCA>
A;Cross-references: GB:M24854; NID:g184851; PIDN:AAA53507.1; PID:g306930
R;Peltz, G.A.; Grundy, H.O.; Lebo, R.V.; Yssel, H.; Barsh, G.S.; Moore, K.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 1013-1017, 1989
A;Title: Human Fc-gamma-RIII: cloning, expression, and identification of the chromosomal location.
A;Reference number: A31460; MUID:89128838; PMID:2521732
A;Accession: A31460
A;Molecule type: mRNA
A;Residues: 1-35,'R',37-64,'N',66-81,'D',83-105,'V',107-233 <PEL>
A;Cross-references: GB:J04162; NID:g183036; PIDN:AAA35881.1; PID:g183037
C;Comment: This low affinity IgG Fc receptor of neutrophils, which is the product of the FCGR3 gene, maps to chromosome 1.
I, yet this receptor lacks 21 residues at the carboxyl end because of an early stop codon.
C;Genetics:
A;Gene: GDB:FCGR3B; FCG3; FCGR3
A;Map position: 1q23-q23
A;Cross-references: GDB:128176; OMIM:146740
A;Introns: 14/1; 21/1
A;Note: the list of introns is incomplete
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkage
F;1-18/Domain: signal sequence.#status predicted <SIG>
F;19-203/Product: Fc gamma (IgG) receptor III-B #status predicted <MAT>
F;40-91/Domain: immunoglobulin homology <IMMI>
F;111-174/Domain: immunoglobulin homology <IMMW>
F;56,63,82,92,180,187/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;203/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form)

Query Match 9.3%; Score 292; DB 1; Length 233;
Best Local Similarity 35.5%; Pred. No. 1.6e-12;
Matches 83; Conservative 34; Mismatches 99; Indels 18; Gaps 10;

QY / 1 MLNWILLVLAPVSQGSPARTPRPIIFLPPTTVTFQGERVTLTCKGFYSPQ--KTKWY 58
Db ||| |||| | | | : : : : : | : : : : | : : : : | : : : : | : : : :
4 LLUPTALLLVLSAGMTEDLPKAVVFLEPQMYSLVKDSVTLKKCG--AYSIEDNSTQWP 61
QY 59 HRVLGKEILRETPDNII-----EVQSEGYRCQAQSPLSSPVHLDFSSASLIQLAPLSVF 114
Db | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
62 H---NESLISSQASYFDIAATVNDSDGEYRCQTNLSTLSDPVLEHVHGWLLQLAPRWPF 118
QY 115 -EGSVVLRCAKAEVTLNTITY-KNDNVLAFLNKRTDFPHIACLKNKONGAYRCTGYKES 172
Db | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
119 KEEDPIHLRCHSWKNALHKVYLQNGDKRKYFHNSDFHIPKATLKDSGSYFCRLGVGS 178
QY 173 CCPVSNNTVIQVEPTRPVRVLASSFPISGNPVTLTCETQLSLERSDVPLRF 226
Db |||| | | | | | | | | | | | | | | : : : : : | : : : : | : : : :
179 -KNVSNSETVNITIQGLA---VSTISSFSF-PGYQVSF-CLVMVLLFAVDGTGLYF 227

JW0284

Fc gamma (IgG) receptor III-B precursor (neutrophil) - human
 N;Alternate names: FcR III; IgG Fc receptor precursor, type III-1 (polymorphonuclear granulocyte)
 C;Species: Homo sapiens (man)
 C;Date: 07-Sep-1990 #sequence revision 02-Aug-1996 #text_change 09-Jul-2004
 C;Accession: J00284; S00758; I37628; B32933; A31460
 R;Ravetch, J. V.; Perussia, B.
 J. Exp. Med. 170, 481-497, 1989
 A;Title: Alternative membrane forms of Fc gamma RII (CD16) on human natural killer cells
 A;Reference number: J0107; MUID:89328325; PMID:2526846
 A;Accession: J00284
 A;Molecule type: mRNA
 A;Residues: 1-201.'SP'.204-233 <RAV>

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RESULT 10
Fc gamma (IgG) receptor - human
S06946
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C:Accession: S06946
R:Stuart, S.G.; Simister, N.E.; Clarkson, S.B.; Kacinski, B.M.; Shapiro, M.; Mellman, I.
EMBO J. 8, 3657-3666, 1989
A:Title: Human IgG Fc receptor (hFCRII; CD32) exists as multiple isoforms in macrophages
A:Reference number: S06946; MUID:90059965; PMID:2531080
A:Accession: S06946
A:Molecule type: mRNA
A:Residues: 1-323 <STU>
A:Cross-references: UNIPROT:P31995; EMBL:X17652; NID:G32073; PIDN:CAA35642.1; PID:G32074
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: immunoglobulin receptor; transmembrane protein
F:64-115/Domain: immunoglobulin homology <IMM>

Query Match 9.3%; Score 290; DB 2; Length 323;
Best Local Similarity 36.3%; Pred. No. 3.2e-12;
Matches 74; Conservative 26; Mismatches 84; Indels 20; Gaps 6;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSQKTKWYHR 60
DB 28 MLLWTAFLVLPVAGTAPPAAPKAVLKLEPQWLVQLQEDSVTLTCRGTSPESDSIQWFHN 87
QY 61 YLGEILRETPDNI---LEVOESGEYRCQAQGSPLSPVHLDFFSSASLILOAP-LSVFEG 116
DB 88 --GNLIPHTQPSYRFKANNNDSEYTCQTGSLSDPVHLVLSWLVLTQPHLEFQEG 145
QY 117 DSVVLCRA-KAEVTLNNTIYKNDVLAFLNKTDFHPIHACLKONGAYRCTG-----Y 169
DB 146 ETIVLRCHSWKDKPLVKVTFFQNGSKKFSRSDPNFISIPQANHSHSGDYHCTGNIGYTL 205
QY 170 KESCCVPSSNTVKIQOEPTRPV 193
DB 206 -----SSKPEVTITVQAPSSSPM 222

RESULT 11
Fc gamma (IgG) receptor IIB precursor - human
JL0119
A:Alternate names: Fc gamma (IgG) receptor II (low affinity) beta; surface glycoprotein
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JL0119; A43543; A60568; A45877; S00478
R:Brooks, D.G.; Qiu, W.Q.; Luster, A.D.; Ravetch, J.V.
J. Exp. Med. 170, 1369-1385, 1989
A:Title: Structure and expression of human IgG FcRII (CD32): functional heterogeneity is
A:Reference number: JL0119; MUID:90010791; PMID:2529342
A:Accession: JL0119
A:Molecule type: mRNA
A:Residues: 1-310 <BRO>
A:Cross-references: UNIPROT:P31994
R:Engelhardt, W.; Geerts, C.; Frey, J.
Eur. J. Immunol. 20, 1367-1377, 1990
A:Title: Distribution, inducibility and biological function of the cloned and expressed
A:Reference number: A43543; MUID:90316181; PMID:2142460
A:Accession: A43543
A:Molecule type: mRNA
A:Residues: 1-204, 'Y', 206-254, 274-310 <ENG>
A:Cross-references: GB:X52473; NID:G3928171; PIDN:CAA36713.1; PID:G29428
R:Engelhardt, W.; Geerts, C.; Frey, J.
Mol. Immunol. 27, 379-382, 1990
A:Title: Organization of human FcRII and FcRII-like (betaFCRII) genes: structural homolo
A:Reference number: A60568; MUID:90294837; PMID:2141667
A:Accession: A60568
A:Molecule type: DNA
A:Residues: 1-38 <EN2>
R:Seki, T.
Immunogenetics 30, 5-12, 1989
A:Title: Identification of multiple isoforms of the low-affinity human IgG Fc receptor.
A:Reference number: A45877; MUID:89307398; PMID:2526077
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A:Accession: A45877
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-74, 'Q', 76-119, 'V', 121-204, 'Y', 206-231, 'T', 233-254, 274-310 <SEK>
A:Cross-references: GB:M28696; NID:G184843; PIDN:AAA36051.1; PID:G306929
A:Note: the authors translated the codon CAG for residue 75 as His
R:Stengelin, S.; Stamenkovic, I.; Seed, B.
EMBO J. 7, 1053-1059, 1988
A:Title: Isolation of cDNAs for two distinct human Fc receptors by ligand affinity clonin
A:Reference number: S00477; MUID:88296409; PMID:3402431
A:Accession: S00478
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-35, 'S', 37-204, 'Y', 206-253, 'G', 255 <STE>
A:Note: the authors suggest that the cDNA is derived from a precursor RNA that still cont
C:Genetics:
A:Gene: GDB:FCGR2B; FCG2; FCGR2
A:Cross-references: GDB:128183; OMIM:146790
A:Map position: 1q23-1q23
A:Introns: 131/1
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: alternative splicing; glycoprotein; immunoglobulin; immunoglobulin receptor;
F:1-44/Domain: signal sequence #status predicted <SIG>
F:45-310/Product: IgG Fc receptor IIB #status predicted <MAT>
F:64-222/Domain: extracellular #status predicted <EXT>
F:64-115/Domain: immunoglobulin homology <IMM1>
F:145-198/Domain: immunoglobulin homology <IMM2>
F:223-245/Domain: transmembrane #status predicted <TMM>
F:246-310/Domain: intracellular #status predicted <INT>
F:246-180,187/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.3%; Score 289; DB 2; Length 310;
Best Local Similarity 36.9%; Pred. No. 3.6e-12;
Matches 73; Conservative 26; Mismatches 91; Indels 8; Gaps 5;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSQKTKWYHR 60
DB 28 MLLWTAFLVLPVAGTAPPAAPKAVLKLEPQWLVQLQEDSVTLTCRGTSPESDSIQWFHN 87
QY 61 YLGEILRETPDNI---LEVOESGEYRCQAQGSPLSPVHLDFFSSASLILOAP-LSVFEG 116
DB 88 --GNLIPHTQPSYRFKANNNDSEYTCQTGSLSDPVHLVLSWLVLTQPHLEFQEG 145
QY 117 DSVVLCRA-KAEVTLNNTIYKNDVLAFLNKTDFHPIHACLKONGAYRCTGKYKESCCP 175
DB 146 ETIVLRCHSWKDKPLVKVTFFQNGSKKFSRSDPNFISIPQANHSHSGDYHCTGNIGYTL 204
QY 176 VSSNTVKIQOEPTRPV 193
DB 205 FSKPEVTITVQAPSSSPM 222

RESULT 12
I38346
elastic titin - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I38346
R:Labeit, S.; Kolmerer, B.
Science 270, 293-296, 1995
A:Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A:Reference number: A57430; MUID:96026330; PMID:7569978
A:Accession: I38346
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-7962 <RES>
A:Cross-references: UNIPROT:Q10465; EMBL:X90569; NID:G1017426; PIDN:CAA62189.1; PID:G101
C:Genetics:
A:Gene: GDB:TTN
A:Cross-references: GDB:127867; OMIM:188840
A:Map position: 2q31-2q31

Query Match 8.8%; Score 275; DB 2; Length 7962;
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Dd 38 LCLSVFVSRVLTLRSPGAQAAVGDLLELHCEALRGSPILYQFYVHDVTLGNSAPSGG 97

Qy 431 GVAISFLTAEHSGNYCYCTADNGFGPQRKSNVSLSTVP 469

Dd 98 GASFNLSLTAEHSNGSYSCANNGLGAQCSEAVPVSISSGP 136

RESULT 14

S00682

IgE Fc receptor alpha chain precursor - human
N/Alternate names: Fc-epsilon receptor
C/Species: Homo sapiens (man)
C/Date: 31-Dec-1988 #sequence revision 31-Dec-1988 #text_change 09-Jul-2004
C/Accession: S00682; B30154; S42209
R/Kochan, J.; Pettine, L.F.; Hakimi, J.; Kishi, K.; Kinet, J.P.
Nucleic Acids Res. 16, 3584, 1988
A>Title: Isolation of the gene coding for the alpha subunit of the human high-affinity IgE Fc receptor
A/Reference number: S00682; MUID:88233953; PMID:2967464
A/Accession: S00682
A/Molecule type: mRNA
A/Residues: 1-257 <CON>
A/Cross-references: UNIPROT:P12319; EMBL:X06948; NID:g31317; PIDN:CAA30025.1; R/Shimizu, A.; Tepler, I.; Benfey, P.N.; Berenstein, E.H.; Siraganian, R.P.; Proc. Natl. Acad. Sci. U.S.A. 85, 1907-1911, 1988
A>Title: Human and rat mast cell high-affinity immunoglobulin E receptors: characterization and cloning
A/Reference number: A94191; MUID:88158102; PMID:2964640
A/Accession: B30154
A/Molecule type: mRNA
A/Residues: 1-257 <SHI>
A/Cross-references: GBJ03605; NID:g187449; PIDN:AAA36204.1; PID:g307164 R/Yagi, S.; Yanagida, M.; Tanida, I.; Hasegawa, A.; Okumura, K.; Ra, C. Eur. J. Biochem. 220, 593-598, 1994
A>Title: High-level expression of the truncated alpha chain of human high-affinant product.
A/Reference number: S42209; MUID:94170811; PMID:8125119
A/Accession: S42209
A/Molecule type: protein
A/Residues: 26-197 <YAG>
A/Experimental source: purified recombinant protein
C/Genetics:
A/Gene: GDB:FCERIA
A/Cross-references: GDB:l119902; OMIM:147140
A/Mapp position: lq23-lq23
C/Superfamily: Fc gamma receptor III; immunoglobulin homology
C/Keywords: Immunoglobulin receptor; transmembrane protein
F/l,1-25/Domain: signal sequence #status predicted <SIG>
F/26-257/Product: IgE Fc receptor alpha chain #status predicted <NAT>
F/44-95/Domain: immunoglobulin homology <IMM1>
F/125-178/Domain: immunoglobulin homology <IMM2>

Query Match 8.5%; Score 267; DB 2; Length 257;
Best Local Similarity 37.0%; Pred. No. 8.4e-11;
Matches 64; Conservative 26; Mismatches 73; Indels 10; Gaps

Qy 2 LLWVILLVLAPVSGGFARTPRPIIFLOPPWTTVFOGERVTLTKCFRPYSPOKTWYHYR 61

Dd 10 LUCVALLFPAP-DGVLAVPQPKVSLNPENPNRIKGNVNTLCNGNNFFVSSTKWHF-- 61

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Qy 62 LGKEILRETPDNI-LEVOSSGEYRCOAQSGPLSSPVHLDFFSSASLILOAPLS-VPEG 11
Db 67 -NGSLSEETNSSINIVNAKFDSGEYKQHQHQWNESEPVYLEVFSDWLLQLQASAEVMEG 12
Qy 117 DSVLFRCAKAEVTLNTI-YKNDNVLAFLNKRDTDFHIPHACLKDKNGAYRCTG 168
Db 126 QPLFLRCHGRWVDVYKVIIYKDGALKVYWNHNHSITNATVEDSGTYCYCTG 178

RESULT 15
JL0118
Fc gamma (IgG) receptor Iia precursor - human
N;Alternate names: Fc gamma (IgG) receptor II (low affinity) alpha; surface g
C;Species: Homo sapiens (man)

```

us-09-724-254a-3.rpr

Thu May 5 15:10:59 2005

C>Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 09-Jul-2004
 A:Accession: J10118; A31932; S02297; B45877; S00477; S02296
 R:Brooks, D.G.; Qiu, W.Q.; Luster, A.D.; Ravetch, J.V.
 J. Exp. Med. 170, 1369-1385, 1989
 A>Title: Structure and expression of human IgG FcRII (CD32): functional heterogeneity is
 A:Reference number: J10118; PMID:90010791; PMID:2529342
 A:Accession: J10118
 A:Molecule type: mRNA
 A:Residues: 1-317 <BRO>
 A:Cross-references: UNIPROT:P12318; GB:M31932; NID:g182473; PIDN:AAA35827.1; PID:g182474
 A:Experimental source: placenta
 A>Note: it is uncertain whether Met-1, Met-3, or Met-7 is the initiator
 R:Hibbs, M.L.; Bonadonna, L.; Scott, B.M.; McKenzie, I.F.C.; Hogarth, P.M.
 Proc. Natl. Acad. Sci. U.S.A. 85, 2240-2244, 1988
 A>Title: Molecular cloning of a human immunoglobulin G Fc receptor.
 A:Reference number: S02296; PMID:88176920; PMID:2965389
 A:Accession: A31932
 A:Molecule type: mRNA
 A:Residues: 3-317 <HIB>
 A:Cross-references: EMBL:J03619; NID:g183619; PIDN:AAA35932.1; PID:g306803
 R:Stuart, S.G.; Irounstone, M.L.; Vaux, D.J.T.; Koch, T.; Martens, C.L.; Mellman, I.; Mc
 J. Exp. Med. 166, 1668-1684, 1987
 A>Title: Isolation and expression of cDNA clones encoding a human receptor for IgG (Fc-
 A:Reference number: S02297; PMID:88061079; PMID:2824655
 A:Accession: S02297
 A:Molecule type: mRNA
 A:Residues: 1, 'T', 3-317 <STU>
 A:Cross-references: EMBL:Y00644; NID:g31335; PIDN:CAA68672.1; PID:g31336
 A>Note: it is uncertain whether Met-1 or Met-7 is the initiator
 R:Seki, T.
 Immunogenetics 30, 5-12, 1989
 A>Title: Identification of multiple isoforms of the low-affinity human IgG Fc receptor.
 A:Reference number: A45877; PMID:89307398; PMID:2526077
 A:Accession: B45877
 A:Molecule type: mRNA
 A:Residues: 7-317 <SEK>
 A:Cross-references: GB:M28697; NID:g184841; PIDN:AAA36050.1; PID:g306928
 R:Stengelin, S.; Stamenkovic, I.; Seed, B.
 EMBO J. 7, 1053-1059, 1988
 A>Title: Isolation of cDNAs for two distinct human Fc receptors by ligand affinity cloni
 A:Reference number: S00477; PMID:88296409; PMID:3402431
 A:Contents: clone PC23
 A:Accession: S00477
 A>Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 7-317 <STE>
 C:Genetics:
 A:Gene: GDB:FCGR2A
 A:Cross-references: GDB:119903; OMIM:146790
 A:Map position: 1q23-1q23
 C:Superfamily: Fc gamma receptor III; immunoglobulin homology
 C:Keywords: glycoprotein; immunoglobulin receptor; transmembrane protein
 F:1-35/Domain: signal sequence #status predicted <SIG>
 F:36-217/Product: IgG Fc receptor IIA #status predicted <REI>
 F:36-216/Domain: extracellular #status predicted <EXT>
 F:36-216/Domain: immunoglobulin homology <IMM1>
 F:55-106/Domain: immunoglobulin homology <IMM2>
 F:136-189/Domain: transmembrane #status predicted <TM>
 F:217-240/Domain: intracellular #status predicted <INT>
 F:241-317/Domain: intracellular #status predicted <INT>
 F:97,178/Binding site: carbohydrate (Asn) #status predicted

Query Match 8.5%; Score 264.5; DB 2; Length 317;
 Best Local Similarity 35.7%; Pred. No. 1.6e-10;
 Matches 70; Conservative 25; Mismatches 88; Indels 13; Gaps 6;
 QY 3 LWV-----ILLVLAPVSGQPARTPRPIIFLQPPWTVFQGERVTLCKGFREYSPQKTKW 57
 Db 16 LMLLQPLTVLLLASADSQAAPKAVLKLPPINVLQEDSVTLTCQARSPESDSIQW 75
 QY 58 YHYLGEIILREPDNI---LEQESGEYRCQAQGSPLSPVHLPDSSASLIQAP-LSV 113
 Db 76 FHN--GNLIPHTQPSYRFKANNNDSEYTCGTQSLSDPPVHLTVLSEWLVLTQPHLEF 133

QY 114 FEGDSVLRCA-KAEVTINNTIYKNDNLAFINLKRTRDFHPIHACLKNDGAYRCTGYKES 172
 Db 134 QEGETIMLRCHSWKDKPLVKVTFQNGKSKQFSLDPTFSIPOANHSYHSHGCTG-NIG 192
 QY 173 CCPVSSNTVKIQVQEP 188
 Db 193 YTLFSSKPVTVITVQVP 208

Search completed: May 4, 2005, 11:39:18
 Job time : 20.5636 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:23:49 ; Search time 79.8488 Seconds
(without alignments)
3796.562 Million cell updates/sec

Title: US-09-724-254A-3
Perfect score: 3124
Sequence: 1 MLLWVILLVLPVSGQFART.....AEPSLTHSFKNLFALESFLP 592

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2949	94.4	977	2 Q96RD9	Q96RD9 homo sapien
2	1193.5	38.2	734	2 Q96LA4	Q96LA4 homo sapien
3	1193.5	38.2	734	2 Q96P31	Q96P31 homo sapien
4	1193.5	38.2	742	2 Q8NGS2	Q8NGS2 homo sapien
5	1186.5	38.0	740	2 Q96P29	Q96P29 homo sapien
6	927.5	29.7	582	2 Q80WN2	Q80WN2 mus musculus
7	927.5	29.7	595	2 Q68SN8	Q68SN8 mus musculus
8	847.5	27.1	639	2 Q96P30	Q96P30 homo sapien
9	826.5	26.5	515	2 Q96P75	Q96P75 homo sapien
10	820.5	26.3	515	2 Q96RE0	Q96RE0 homo sapien
11	773.5	24.8	508	2 Q96LA5	Q96LA5 homo sapien
12	772	24.7	360	2 Q8N732	Q8N732 homo sapien
13	692.5	22.2	508	2 Q8BJA5	Q8BJA5 mus musculus
14	657.5	21.0	437	2 Q8NF56	Q8NF56 homo sapien
15	600.5	19.2	509	2 Q9EQV5	Q9EQV5 m mman-g pr
16	599.5	19.2	509	2 Q91VK7	Q91VK7 mus musculus
17	565	18.1	428	2 Q96P76	Q96P76 homo sapien
18	565	18.1	429	2 Q96LA6	Q96LA6 homo sapien
19	548	17.5	124	2 Q6UY46	Q6UY46 homo sapien
20	548	17.5	366	2 Q8N759	Q8N759 homo sapien
21	543.5	17.4	154	2 Q8N733	Q8N733 homo sapien
22	537.5	17.2	422	2 Q96P73	Q96P73 homo sapien
23	452	14.5	722	2 Q6GNB3	Q6GNB3 xenopus lae
24	448.5	14.4	426	2 Q6BAA4	Q6BAA4 homo sapien
25	446.5	14.3	626	2 Q6DCH3	Q6DCH3 xenopus lae
26	428.5	13.7	357	2 Q8SPW5	Q8SPW5 macaca fasc
27	418.5	13.4	374	1 FCG1 HUMAN	P12314 homo sapien
28	402.5	12.9	372	2 Q7YQJ5	Q7YQJ5 canis famil
29	402.5	12.9	404	1 FCG3_MOUSE	P26151 mus musculus
30	396	12.7	330	2 Q8R142	Q8R142 mus musculus
31	369	11.8	349	2 Q9M2T0	Q9M2T0 bos taurus

RESULT 1

ID	Q96RD9	PRELIMINARY;	PRT;	977 AA.
AC	Q96RD9;			
DT	01-DEC-2001 (Tremblrel. 19, Created)			
DT	01-DEC-2001 (Tremblrel. 19, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	Fc receptor-like protein 5.			
GN	Names=FCRH5;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21396562; PubMed=11493702; DOI=10.1073/pnas.171308498;			
RA	David R.S., Wang Y.H., Kubagawa H., Cooper M.D.;			
RT	"Identification of a family of Fc receptor homologs with preferential B cell expression."			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777(2001).			
DR	EMBL; AF397453; AAK93971.1; .			
DR	HSSP; P12319; 1P2Q.			
DR	GO; GO:0004872; Fireceptor activity; IEA.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003598; Ig_c2.			
DR	Pfam; PF00047; Ig; 8.			
DR	SMART; SM00408; Igc2; 1.			
DR	PROSITE; PS50835; IG_LIKE; 8.			
KW	Receptor.			
SQ	SEQUENCE 977 AA; 106496 MW; 24E4A027B25509E7 CRC64;			

Query Match 94.4%; Score 2949; DB 2; Length 977;

Best Local Similarity 98.3%; Pred. No. 4.6e-204;

Matches 562; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

QY	1	MLLWVILLVLPVSGQFARTPRPIIFLQPPWTVFQGERVTLTKGFRFYSPQTKWYHR	60
Db	1	MLLWVILLVLPVSGQFARTPRPIIFLQPPWTVFQGERVTLTKGFRFYSPQTKWYHR	60
QY	61	YLKKEILRETPDNILVQESGEYRCQAQSPVHLPFSSASLILOAPLSVFEQDSVV	120
Db	61	YLKKEILRETPDNILVQESGEYRCQAQSPVHLPFSSASLILOAPLSVFEQDSVV	120
QY	121	LRCRAAEVTLNNTIYKNDVLAFLNKRITDFHIFHACLKNDGAYRCTGYKESCCPVSSNT	180
Db	121	LRCRAAEVTLNNTIYKNDVLAFLNKRITDFHIFHACLKNDGAYRCTGYKESCCPVSSNT	180
QY	181	VKIQQEPTPRVLRASSFPISGNEPVTLTCTQLSLERSDVPFLRFRFRDDQTLGLGWS	240
Db	181	VKIQQEPTPRVLRASSFPISGNEPVTLTCTQLSLERSDVPFLRFRFRDDQTLGLGWS	240
QY	241	LSPNFOITAMWSKDSGFYCKAATMPHSVISDSPRSWIQVQIPASHPVLTLSPEKALNFE	300
Db	241	LSPNFOITAMWSKDSGFYCKAATMPHSVISDSPRSWIQVQIPASHPVLTLSPEKALNFE	300

QY	301	GTGKTLHCEQDSRLTYRPFYHGVPLRHKSVRCERGASISFSLTTSNGNYCTADNG	360
Db	301	GTGKTLHCEQDSRLTYRPFYHGVPLRHKSVRCERGASISFSLTTSNGNYCTADNG	360
QY	361	LGAKSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA	420
Db	361	LGAKSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA	420
QY	421	LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSA	480
Db	421	LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSA	480
QY	481	EALTFFGATVTLHCEVORSGPOLLYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGNY	540
Db	481	EALTFFGATVTLHCEVORSGPOLLYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGNY	540
QY	541	CTADNGFGPQRSEVWSLFTVGKWLKPL 572	
Db	541	CTADNGFGPQRSEVWSLFTV---VPVSRPIL 568	
RESULT 2			
QY6LA4	Q96LA4	PRELIMINARY; PRT; 734 AA.	
AC	Q96LA4		
DT	01-DEC-2001	(TrEMBLrel. 19, Created)	
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)	
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)	
DE	FC	receptor-like protein 3.	
GN	Name=PCRH3;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21396562; PubMed=11493702; DOI=10.1073/pnas.171308498;		
RA	Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;		
RT	"Identification of a family of Fc receptor homologs with preferential		
RT	B cell expression."		
RL	Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777(2001).		
DR	EMBL; AY043466; AAK91779.1; -.		
DR	HSSP; P12319; IF2Q.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003598; Ig_c2.		
DR	InterPro; IPR002052; N6_Mtase.		
DR	Pfam; PF00047; ig; 4.		
DR	SMART; SM00408; Igc2; 1.		
DR	PROSITE; PS00835; IG_LIKE; 6.		
DR	PROSITE; PS00092; N6_MTASE; UNKNOWN_1.		
KW	Receptor.		
SQ	SEQUENCE 734 AA; 80827 MW; B359B494EBF12138 CRC64;		
Query Match 38.2%; Score 1193.5; DB 2; Length 734;			
Best Local Similarity 45.5%; Pred. No. 1.7e-77;			
Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;			
QY	1	MLLWVILLVAVSGQFARTPRPIIFLOPPWTVTFQGERVTLTKGFRFYSPO-KTKWYH 59	
Db	1	MLLWVILLVAVSGQFARTPRPIIFLOPPWTVTFQGERVTLTKGFRFYSPO-KTKWYH 59	
QY	60	RYLGKILRETPNILEVQESGEYRCQAQSGPLSPVHLDFSSASLIIQAPLSVFEQDSV 119	
Db	60	RYLGKILRETPNILEVQESGEYRCQAQSGPLSPVHLDFSSASLIIQAPLSVFEQDSV 119	
QY	61	---DEKLLTKKHDKI-QITEPGNYCKTRGSSLSDAVHVEFSPDWLLIQLALHPVFEQDNV 116	
Db	61	---DEKLLTKKHDKI-QITEPGNYCKTRGSSLSDAVHVEFSPDWLLIQLALHPVFEQDNV 116	
QY	120	VLCRAKAEVTLNNTIYKNDNVLAFLNKRDTFPHIACLKONGAYRCTGYKESC---CPV 176	
Db	120	VLCRAKAEVTLNNTIYKNDNVLAFLNKRDTFPHIACLKONGAYRCTGYKESC---CPV 176	
QY	177	SSNTVKIQOEPFTRPVLRASSPOISGNPVTITCETQLSLERSDVPLRFRFRDQTIG 236	
Db	177	SSNTVKIQOEPFTRPVLRASSPOISGNPVTITCETQLSLERSDVPLRFRFRDQTIG 236	
QY	177	TSKPLNIQVQELFLHPLVRASSSTPIEGSPMTITCETQLSPQRPDVQLQFSLFRDSTQLG 236	
Db	177	TSKPLNIQVQELFLHPLVRASSSTPIEGSPMTITCETQLSPQRPDVQLQFSLFRDSTQLG 236	
QY	237	LGWISLPNQTITAMSKDGGFWCAATPHSVISDSRSMIOVO-IPASHPVLTLSPEK 295	
Db	237	LGWISLPNQTITAMSKDGGFWCAATPHSVISDSRSMIOVO-IPASHPVLTLSPEK 295	
QY	296	ALNFEGTKVTLHCEQDSRLTYRPFYHGVPLRHKSVRCERGASISFSLT---ENSGN 352	
Db	296	ALNFEGTKVTLHCEQDSRLTYRPFYHGVPLRHKSVRCERGASISFSLT---ENSGN 352	
QY	353	YYCTADNGILGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILY 412	
Db	353	YYCTADNGILGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILY 412	
QY	413	QFHEDAAALERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSIITVPVSH 472	
Db	413	QFHEDAAALERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSIITVPVSH 472	
QY	473	PVLTLSAEALTFEGATVTLHCEVORSGPOLLYQFYHEDMPLVSSSTPSVGRVSFSLT 532	
Db	473	PVLTLSAEALTFEGATVTLHCEVORSGPOLLYQFYHEDMPLVSSSTPSVGRVSFSLT 532	
QY	533	EGHSGNYCTADNGFGPQRSEVWSLFTVG 561	
Db	533	EGHSGNYCTADNGFGPQRSEVWSLFTVG 561	
QY	536	TEHSGNYCEADNGLGAQHSKVVTILNVG 564	
Db	536	TEHSGNYCEADNGLGAQHSKVVTILNVG 564	
RESULT 3			
QY6P31	Q96P31	PRELIMINARY; PRT; 734 AA.	
AC	Q96P31		
DT	01-DEC-2001	(TrEMBLrel. 19, Created)	
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)	
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)	
DE	SH2	domain-containing phosphatase anchor protein 2a.	
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Xu M.-J., Zhao R., Zhao Z.J.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF416901; AAL13290.1; -.		
DR	HSSP; P12319; IF2Q.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003598; Ig_c2.		
DR	InterPro; IPR002052; N6_Mtase.		
DR	Pfam; PF00047; ig; 4.		
DR	SMART; SM00408; Igc2; 1.		
DR	PROSITE; PS00835; IG_LIKE; 6.		
DR	PROSITE; PS00092; N6_MTASE; UNKNOWN_1.		
SQ	SEQUENCE 734 AA; 80855 MW; B3411B73A35EC668 CRC64;		
Query Match 38.2%; Score 1193.5; DB 2; Length 734;			
Best Local Similarity 45.5%; Pred. No. 1.7e-77;			
Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;			
QY	1	MLLWVILLVAVSGQFARTPRPIIFLOPPWTVTFQGERVTLTKGFRFYSPO-KTKWYH 59	
Db	1	MLLWVILLVAVSGQFARTPRPIIFLOPPWTVTFQGERVTLTKGFRFYSPO-KTKWYH 59	
QY	60	RYLGKILRETPNILEVQESGEYRCQAQSGPLSPVHLDFSSASLIIQAPLSVFEQDSV 119	
Db	60	RYLGKILRETPNILEVQESGEYRCQAQSGPLSPVHLDFSSASLIIQAPLSVFEQDSV 119	
QY	61	---DEKLLTKKHDKI-QITEPGNYCKTRGSSLSDAVHVEFSPDWLLIQLALHPVFEQDNV 116	
Db	61	---DEKLLTKKHDKI-QITEPGNYCKTRGSSLSDAVHVEFSPDWLLIQLALHPVFEQDNV 116	
QY	120	VLCRAKAEVTLNNTIYKNDNVLAFLNKRDTFPHIACLKONGAYRCTGYKESC---CPV 176	
Db	120	VLCRAKAEVTLNNTIYKNDNVLAFLNKRDTFPHIACLKONGAYRCTGYKESC---CPV 176	
QY	177	SSNTVKIQOEPFTRPVLRASSPOISGNPVTITCETQLSLERSDVPLRFRFRDQTIG 236	
Db	177	SSNTVKIQOEPFTRPVLRASSPOISGNPVTITCETQLSLERSDVPLRFRFRDQTIG 236	
QY	177	TSKPLNIQVQELFLHPLVRASSSTPIEGSPMTITCETQLSPQRPDVQLQFSLFRDSTQLG 236	
Db	177	TSKPLNIQVQELFLHPLVRASSSTPIEGSPMTITCETQLSPQRPDVQLQFSLFRDSTQLG 236	

DR PROSITE; PS50835; IG LIKE; 6.
 DR PROSITE; PS00092; N6_WTASE; UNKNOWN 1.
 SQ SEQUENCE 740 AA; 81440 MW; 038AF8A3A2909E46 CRC64;
 Query Match 38.0%; Score 1186.5; DB 2; Length 740;
 Best Local Similarity 45.2%; Pred. No. 5.4e-77;
 Matches 260; Conservative 75; Mismatches 221; Indels 19; Gaps 8;
 QY 1 MLWLILVAVSGOFARTPRPIIFLOPPPTTTFQGERVTLTCKGFRFYSPQ-KTKWYH 59
 DB 1 MLWLILVAVSGOFARTPRPIIFLOPPPTTTFQGERVTLTCKGFRFYSPQ-KTKWYH 60
 QY 60 RYLKGLRETPDNTILEVQESGEYRCQAQGSPLSPVHLDFFSSASLILOAPLSVPEGSV 119
 DB 61 ---DEKLKIKHDKI-QITEPGNYQCKTRGSSLSDAVHVEFSPDWLILQALHPVEGDNV 116
 QY 120 VLRCRAKAEVTLNNTYKNDVLAFLNKETDHI PHACLKONGAYRCTGYKESC---CPV 176
 DB 117 ILRCQKDNKNTKQYKYYKDGKQLPNSYNLEKIVNSVSRDMSKYHCTAYKFIYLDIEV 176
 QY 177 SNTVTKIQVQEPTRPVLRASSFPQISGNPVTLCETQLSLERSDVPLRFRFRDDQTLG 236
 DB 177 TSXPLNIQVQLFLHPLVLRASSSTPIEGSPMTLCETQLSPQRPVQLQSLFRDSQTLG 236
 QY 237 LGWSLSPNFOITAMWSDGSGFYWCKAATMPHSVIDSPRSWIQVQ-IPASHPVLTLSPK 295
 DB 237 LGWSRSPRLQIPAMNTEDSGSYWCEVETVTHSIKKRSLRSQIRVQRPVSNVNLEIRPTG 296
 QY 296 ALNFEGTKVTLHCETQEDSLRTLRYRHYEGVPLRHKSVCRCGASISFSLTT---ENSG 352
 DB 297 GQIEGENWVLLICSVAGSGTTFVSHKEG-RVSLGRKTQSLLAELHLVLTAKESDAGR 355
 QY 353 YYCTADN-----GLGAKPKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRG 406
 DB 356 YYCAADNVHSPILSTWIRVTVTLTLLSPVSHPVNLTFRAPRAHTVVGDLLELHCESLRG 415
 QY 407 SLPLIYOFHEDHAALERSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVLSLI 466
 DB 416 SPPLIYRFYHEDVTLGNSSAPSGGGASFNLSLTAHSGNYSCDADNGLGAQHSHGVSLRV 475
 QY 467 TVPVSHPVLTLSAEALTTFEGATVTLHCEVQGRSPQILYOFHEDMPLVSSSTPPSGRVS 526
 DB 476 TVPVSRLVTLRAGAAVGDLELHCESLRGSPILYWFYHEDDITLGNISAHSGGAS 535
 QY 527 FSLTGHSGNYCTADNGFGPQRSEVSLFTVG 561
 DB 536 FNLSTLTHSGNYSCEADNGLGAQHSHGVTLNVTG 570
 RESULT 6
 Q80WN2 PRELIMINARY; PRT; 582 AA.
 ID Q80WN2
 AC Q80WN2;
 DT 01-JUN-2003 (TremBLrel. 24, Created)
 DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
 DE BXMASI-like protein 2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RL Nakayama Y., Maher S.E., Weissman S.M., Bothwell A.L.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY158090; AAO20873.1;
 DR HSSP; P12319; 1F2Q.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00408; Igc2; 2.
 DR PROSITE; PS50835; IG LIKE; 5.
 SQ SEQUENCE 582 AA; 65248 MW; 44321E93FB9EDF06 CRC64;
 Query Match 29.7%; Score 927.5; DB 2; Length 582;
 Best Local Similarity 41.9%; Pred. No. 2e-58;
 Matches 209; Conservative 82; Mismatches 161; Indels 47; Gaps 9;
 QY 3 LWLILVAVSGOFARTPRPIIFLOPPPTTTFQGERVTLTCKGFRFYSPQKTKWYHRL 62
 DB 1 MWLILVAVSGOFARTPRPIIFLOPPPTTTFQGERVTLTCKGFRFYSPQKTKWYHRL 62
 QY 63 GKEILRETPD-----NILEVQESGEYRCQAQGSPLSPVHLDFFSSASLILOAPLSVFE 116
 DB 59 -RKTVKTPCALVIKHAHTLKVESGEYWCADSLSPSMHVNVEFSEDFVLQAPPAVFE 117
 QY 117 DSVLRCRAKAEVTLNNTYKNDVLAFLNKETDHI PHACLKONGAYRCTGYKESC--- 173
 DB 118 DSVLRCYAKKGEAEVTLTYKDGKALT-LHSGELSIHANLKDNGOYKCTSKKWSFG 176
 QY 174 CPVSSNTVTKIQVQEPTRPVLRASSFPQISGNPVTLCETQLSLERSDVPLRFRFRDDQ 233
 DB 177 SLYTSNTVGVQVQLFPRPVLRASSPIDGSPVTLTCTQLSAQKSDARLQCFPRNLQ 236
 QY 234 TLGLGWSLSPNFOITAMWSDGSGFYWCKAATMPHSVIDSPRSWIQVQIPASHPVLTLSP 293
 DB 237 LLGSGCSRSEFEHIPAITEESRYOQCAETVNSQVRKQSTAFIIPVORASAPFTHIIP 296
 QY 294 EKALNFGTKVTLHCETQEDSLRTLRYRHYEGVPLRHKSVCRCGASIS 342
 DB 297 ASKLVFEGQLLLNCV-----KGVPGLKFSWYKMDLNEETKILKSSNAE 343
 QY 343 FSLTATEN---SGNYCTADNGLGAKPKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTL 399
 DB 344 FKISQWISDAGEVHCEATNSRFSVSRAPFITIKVPVQFVLTSLTGTQALDEGLDML 403
 QY 400 HCEAQRGSLPILYOFHEDHAALERSANSAGGVAISFSLTAHSGNYCTADNGFGPQR 459
 DB 404 HCQQRGSPCILYBFFVENYVNSGSIILSGGAYFNFSMSTERSGNYCTADNGLGAQCS 463
 QY 460 KAVLSLI-----TVPVS 471
 DB 464 EAIRISIFDMTKNRSVPMA 482
 RESULT 7
 Q68SN8 PRELIMINARY; PRT; 595 AA.
 ID Q68SN8
 AC Q68SN8;
 DT 25-OCT-2004 (TremBLrel. 28, Created)
 DT 25-OCT-2004 (TremBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TremBLrel. 28, Last annotation update)
 DE Fc receptor-like protein 3.
 GN Name=Fcrh3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Spleen;
 RL PubMed=15302849;
 RA Davis R.S., Stephan R.P., Chen C.C., Dennis G. Jr., Cooper M.D.;
 RL "Differential B cell expression of mouse Fc receptor homologs";
 RL Int. Immunol. 16:1343-1353(2004).
 DR EMBL; AY506558; AAS91578.1;
 DR GO; GO:004872; Fc receptor activity; IEA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00409; IG; 5.
 DR SMART; SM00408; Igc2; 4.
 DR PROSITE; PS50835; IG LIKE; 5.
 KW Receptor.


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SQ SEQUENCE 595 AA; 66619 MW; 6ABEDB8E2F6AFACE CRC64;
Query Match 29.7%; Score 927.5; DB 2; Length 595;
Best Local Similarity 41.9%; Pred. No. 2e-58;
Matches 209; Conservative 82; Mismatches 161; Indels 47; Gaps 9;

QY 3 LMLVILLVLAPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRFYSPOKTKWYHRL 62
D 14 MMLTLLVVTVPNGOHEAAQSVSLQPPWTTFFRGEVVTLTCTYRFGFSVPQKTKWYQ-- 71
QY 63 GKEILRETPD-----NILEVQESGEYRCQAQSPSLSPVHLDFSSASLILQAPLSVFE 116
D 72 -RKTVKTPGALVIAKHTLKVHESGEYWCQADSLPSMHNVEFSEDFVLQAPPAVFE 130
QY 117 DSVVLRCAKAEVTLNN-TYKNDNVLAFLNKRTHFIHACLDKNGAYRGTGYKESC-- 173
D 131 DSVVLRCAKAEVTLNN-TYKNDNVLAFLNKRTHFIHACLDKNGAYRGTGYKESC-- 173
QY 174 CPVSSNTVKIQVQEPFTRPVLRASSFQIPISGNPVTLTCTQLSLERSDVPRLFRFDD 233
D 190 SLTYSNTVGQVQELFPRLVLRAPSPHIDGSPVTLTCTQLSAQSDARLQFCFFRN 249
QY 234 TLGLGWSLSPNFOITAMWSKDSGYWCKAATMPHSHVSDSPRSWIOVQIPASHVPLTSP 293
D 250 LLSGCSRSSEFHPAIWTESSRYQCAETVNSQVRKQSTAFIIPVORASAPQTHIIP 309
QY 294 EKALNFGKTVLHCETQEDSLRTLYRPFYHEGV-----LRHKSVCRCERGASIS 342
D 310 ASKLIVFEGQLLLNCV-----KGVFGLPKFSWYKMDLNEETKILKSSNAE 356
QY 343 FSLTTE-----SGNYCTADNGLGKPKSKAVSLSVTVVSHVPLNLSPEDLIFEGAKVTL 399
D 357 FKISQVNSIDAGEYHCEATNRRSFRVSRAPFIIKVPVSPVLTSLGKTQALEGLMTL 416
QY 400 HCEAQRGSLPILQFHEDDALERRSANSAGGVAISFLTAHSGNYCTADNGLGKPKS 459
D 417 HCSQRGSPCLLBEFFENYSLGNSILSGGAYNFMSSTERSGNYCTADNGLGKPKS 476
QY 460 KAVLSLSI-----TVPVS 471
D 477 EAIRISIFDNTKRSVPM 495

RESULT 8
Q96P30 PRELIMINARY; PRT; 639 AA.
AC Q96P30
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE SH2 domain-containing phosphatase anchor protein 2b.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RA Xu M.-J., Zhao R., Zhao Z.J.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF16902; AAL1391.1; -.
DR HSSP; P12319; 1F2Q.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR02052; N6_Mtase.
DR Pfam; PF00047; ig_3.
DR SMART; SM00408; Igc2; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.
SQ SEQUENCE 639 AA; 69928 MW; DEAD7AD4E64CA984 CRC64;
Query Match 27.1%; Score 847.5; DB 2; Length 639;
Best Local Similarity 38.4%; Pred. No. 1.3e-52;
Matches 203; Conservative 75; Mismatches 203; Indels 47; Gaps 12;

SQ SEQUENCE 595 AA; 66619 MW; 6ABEDB8E2F6AFACE CRC64;
Query Match 29.7%; Score 927.5; DB 2; Length 595;
Best Local Similarity 41.9%; Pred. No. 2e-58;
Matches 209; Conservative 82; Mismatches 161; Indels 47; Gaps 9;

QY 3 LMLVILLVLAPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRFYSPOKTKWYHRL 62
D 14 MMLTLLVVTVPNGOHEAAQSVSLQPPWTTFFRGEVVTLTCTYRFGFSVPQKTKWYQ-- 71
QY 63 GKEILRETPD-----NILEVQESGEYRCQAQSPSLSPVHLDFSSASLILQAPLSVFE 116
D 72 -RKTVKTPGALVIAKHTLKVHESGEYWCQADSLPSMHNVEFSEDFVLQAPPAVFE 130
QY 117 DSVVLRCAKAEVTLNN-TYKNDNVLAFLNKRTHFIHACLDKNGAYRGTGYKESC-- 173
D 131 DSVVLRCAKAEVTLNN-TYKNDNVLAFLNKRTHFIHACLDKNGAYRGTGYKESC-- 173
QY 174 CPVSSNTVKIQVQEPFTRPVLRASSFQIPISGNPVTLTCTQLSLERSDVPRLFRFDD 233
D 190 SLTYSNTVGQVQELFPRLVLRAPSPHIDGSPVTLTCTQLSAQSDARLQFCFFRN 249
QY 234 TLGLGWSLSPNFOITAMWSKDSGYWCKAATMPHSHVSDSPRSWIOVQIPASHVPLTSP 293
D 250 LLSGCSRSSEFHPAIWTESSRYQCAETVNSQVRKQSTAFIIPVORASAPQTHIIP 309
QY 294 EKALNFGKTVLHCETQEDSLRTLYRPFYHEGV-----LRHKSVCRCERGASIS 342
D 310 ASKLIVFEGQLLLNCV-----KGVFGLPKFSWYKMDLNEETKILKSSNAE 356
QY 343 FSLTTE-----SGNYCTADNGLGKPKSKAVSLSVTVVSHVPLNLSPEDLIFEGAKVTL 399
D 357 FKISQVNSIDAGEYHCEATNRRSFRVSRAPFIIKVPVSPVLTSLGKTQALEGLMTL 416
QY 400 HCEAQRGSLPILQFHEDDALERRSANSAGGVAISFLTAHSGNYCTADNGLGKPKS 459
D 417 HCSQRGSPCLLBEFFENYSLGNSILSGGAYNFMSSTERSGNYCTADNGLGKPKS 476
QY 460 KAVLSLSI-----TVPVS 471
D 477 EAIRISIFDNTKRSVPM 495

RESULT 8
Q96P30 PRELIMINARY; PRT; 639 AA.
AC Q96P30
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE SH2 domain-containing phosphatase anchor protein 2b.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RA Xu M.-J., Zhao R., Zhao Z.J.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF16902; AAL1391.1; -.
DR HSSP; P12319; 1F2Q.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR02052; N6_Mtase.
DR Pfam; PF00047; ig_3.
DR SMART; SM00408; Igc2; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.
SQ SEQUENCE 639 AA; 69928 MW; DEAD7AD4E64CA984 CRC64;
Query Match 27.1%; Score 847.5; DB 2; Length 639;
Best Local Similarity 38.4%; Pred. No. 1.3e-52;
Matches 203; Conservative 75; Mismatches 203; Indels 47; Gaps 12;

QY 1 MMLVILLVLAPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRFYSPOKTKWYH 59
D 1 MMLVILLVLAPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRFYSPOKTKWYH 60
QY 60 RYLGKEILRETPD-----NILEVQESGEYRCQAQSPSLSPVHLDFSSASLILQAPLSVFE 119
D 61 ---DEKLLIKHKDKI-QITEFGNYQCKTRGSSLSDAVHVFSPDWLILQALHPVFE 116
QY 120 VLRCAKAEVTLNNTYKNDNVLAFLNKRTHFIHACLDKNGAYRGTGYKESC--CPV 176
D 117 ILRCQKDNKNTVKQYKDGKQLPNSYNLEKIVNSVRDNSKYHCTARKFYILDIEV 176
QY 177 SSNTVKIQVQEPFTRPV-----LRASSFQIPISGNPVTLTCTQLSLERSDVPRLFRF 230
D 177 TSKPLNIQVQGV---PVSNNVLEIRPTGGQLIEGENMVLIC-----SVAQSGTTFV 229
QY 231 DDQTLGLG-----WSLSPNFOITAMWSKDSGYWCKAATMPHSHVSDSPRSWIO--VO 284
D 230 EGRVSLGRKTQSRSLAELHVLTVKESDAGRYCAADNVHSPILS-----TWIRVT 285
QY 285 SHPVLTLSPEKALNFGKTVLHCETQEDSLRTLYRPFYHEGVPLRHKSVRCERGASIS 344
D 286 SHPVLTFRAPRANTVVGDLLEHCSLRGSPPILYRPFYHEDEVTLGNSAASFGGAS 345
QY 345 LTTENSGNYCTADNGLGKPKSKAVSLSVTVVSHVPLNLSPEDLIFEGAKVTLHCEAQ 404
D 346 LTAHSGNSYCDADNGLGKPKSKAVSLSVTVVSHVPLNLSPEDLIFEGAKVTLHCEAQ 405
QY 405 RGSPLILYQFHEDDALERRSANSAGGVAISFLTAHSGNYCTADNGLGKPKSKAVSL 464
D 406 RGSFPILYFYFHEDDTLGNISAHSGGASFNLSLTTEHSGNSYCEADNGLGKPKSKAV 465
QY 465 SIT-----VPSHVPVLTLSAEALTFFEGATVTLHCEVQGRSP 501
D 466 NVTGTSENRTGLTAAGITGLVLSI-----LVLAALLLHYARARKP 508

RESULT 9
Q96PJ5 PRELIMINARY; PRT; 515 AA.
AC Q96PJ5
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE IFGP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RA TISSUE-Tonsil;
RX MEDLINE=22033006; PubMed=12037601; DOI=10.1007/s00251-002-0436-x;
RA Guseinikov S.V., Brshova S.A., Mechetina L.V., Najakshin A.M.,
RA Volkova O.Y., Alabyev B.Y., Taranin A.V.;
RT "A family of highly diverse human and mouse genes structurally links
RL leukocyte FcR, gp42 and PECAM-1.";
RL Immunogenetics 54:87-95(2002).
DR ENBL; AF329490; AAL23900.1; -.
DR HSSP; P12319; 1F2Q.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig_3.
DR SMART; SM00408; Igc2; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
SQ SEQUENCE 515 AA; 57224 MW; F3B7AD14FB1B449A CRC64;
Query Match 26.5%; Score 826.5; DB 2; Length 515;
Best Local Similarity 43.5%; Pred. No. 3.3e-51;
Matches 184; Conservative 55; Mismatches 161; Indels 23; Gaps 6;

QY 1 MMLVILLVLAPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRFYSPOKTKWYH 60
```

Db	61	HTWGEKLTITPGNTLEVRSGLYRCQARGSPRNPVRLLFSSDSLILQAPYSVFEGLTV	120
Qy	121	LRCKRAEAVTLNNTYK-NDNVIAFLNKRTHPHACLKONGAYRCTGYKESCCPVSSN	179
Db	121	LRCHRRRKEKLTAVKYTWNGNLTISNKSDDLIPQASSNNNGNYRCICYGDENDVFRN	180
Qy	180	TVKIQVOEFTPRPVLRASSFPQISGNPVTLTCTETQLSLERSDVPFRFFRDDQTLGLGW	239
Db	181	FKIIKIQELFPHPELKATDSQTEGNSVNLSCETQLPPERSDTPLFHFNFRDGEVILSDW	240
Qy	240	SLSPNFQITAMWSKSGFYWCXAAATWPHSVISDSRPMIOVQ-IPASHPVLTLSPKALN	298
Db	241	STYPELQLPTVWRENSGSYWCAGETVRGNIHKHSPSLQIHVORIIPVSGVLLLETQSGGQA	300
Qy	299	FEKTKVTLHCETOEDSLRTLYRPFYHEGV-PLRHKSVCRCERGASISFSLTTENSNNYCT	356
Db	301	VEGEMLVLCVSAEGTDTFFSHREDMQESLGRKTQSLRAELELPAIROSHAGGYCT	360
Qy	357	ADNGLGAKPSKAVSLSVTPVSHPVNLSPEDLIFEQA-----KVTLLHCEAQ	404
Db	361	ADNSYG--PVQSMVNLVTVRETP-----GNRDGLVAAGATGGLLSALLLAVALLFHCWRR	413
Qy	405	RGS 407	
Db	414	RKS 416	
RESULT 11			
Db	Q96LA5	PRELIMINARY; PRT; 508 AA.	
Qy	AC Q96LA5;		
DT	01-DEC-2001 (TREMBlrel. 19, Created)		
DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)		
DT	05-JUL-2004 (TREMBlrel. 27, Last annotation update)		
DE	FC receptor-like protein 2 (FcRH2).		
GN	Name=FCRH2; ORFNames=UNQ9236;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21396562; PubMed=11493702; DOI=10.1073/pnas.171308498;		
RA	Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;		
RT	"Identification of a family of Fc receptor homologs with preferential		
RT	B cell expression.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777 (2001).		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21396562; PubMed=12975309; DOI=10.1101/gr.1293003;		
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,		
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,		
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,		
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,		
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,		
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,		
RA	Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,		
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,		
RA	Godowski P.;		
RT	"The secreted protein discovery initiative (SPDI), a large-scale		
RT	effort to identify novel human secreted and transmembrane proteins: a		
RT	bioinformatics assessment.";		
RL	Genome Res. 13:2265-2270 (2003).		
DR	EMBL; AY043465; AAK91778.1; -		
DR	EMBL; AY358130; AAK88497.1; -		
DR	HSP; P12319; IF2Q.		
DR	Genew; HGNC:14875; SPAP1.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	InterPro; IPR007110; Ig-like.		
DR	Pfam; PF00047; Ig; 3.		
DR	PROSITE; PS50835; IG_LIKE; 3.		
KW	Receptor.		
SQ	SEQUENCE 508 AA; 55541 MW; 9AB30E0411B41EDC CRC64;		
Query Match			
Best Local Similarity 43.3%; Pred. No. 8.9e-51;			
Matches 183; Conservative 55; Mismatches 162; Indels 23; Gaps 6;			
Qy	1	MLLWVILLVAPVSGQFARTPRPIIFLPQPPWTTFVQGERVTLTCGFRFPYSPQTKWYHR	60
Db	1	MLLWASLLAFAPVCGQSAAHKPVISVHPPTTFKGERVTLTCNGQFYATEKTTWYHR	60
Qy	61	YLKGEILRETPDNILEVQESGERVRCQAGSPVHLDFSSASLILQAPLSVFEGLTV	120

Query Match 24.8%; Score 773.5; DB 2; Length 508;
 Best Local Similarity 47.3%; Pred. No. 2.1e-47;
 Matches 176; Conservative 46; Mismatches 137; Indels 15; Gaps 6;

QY 104 SLIIQAFLSVEGDSVVLRCRAKAEVTLNNTIYKNDN-VLAFLNKRTPDHPHACLKNDG 162
 DB 19 SLTLVAFSSVFEQDSIVLKQGEQNWIKQWYHKDKNELSVFKFSDFLIQSAVLSDSG 78

QY 163 AYRC-TGYKSCCPVSSNTVKIQVQEPFTRPVLRASSFPQISGNPVTLCETQLSLERSD 221
 DB 79 NYFCSTKGQLFLMDKNTSNIVKIKVQELFQRPVLTASSFPQIEGGPVSCLKETRLSPQRLD 138

QY 222 VPLRFRFRDDQTLGLGWSLSPNQITAMSKDSGFWYCKAATPHSVISDSRSTQVQ 281
 DB 139 VQLQFCFRENQVLGWSWSSPELQISAVWSEDTGYSWYCAETVTHRIKQSLQSIHVQ 198

QY 282 -IPASHPVLTLSPEKALNFEQTKVTLHCETQDSRLTRYFYHE--GVPLRHKSVCRCRG 338
 DB 199 RPIPSNVLSLEIRAPGGQVQTEGQKLILCSVAGGFGNVTFSWYREATGTSNGKKTQR---- 254

QY 339 ASISFSL-----TTENSGNYCTADNGLGAKPKSKAVSLSVTPVSHPVNLSPEDLIPE 393
 DB 255 -SLSAELEIPAVKESDAGKYCRADNGHVPIQSKVNPVPIVSRPVLTLRSPGAQAV 313

QY 394 GAKVTLHCEAQRSLPILYQFHEDALERRSANSAGGVAISFSLTAHSGNYCTADNG 453
 DB 314 GDLELHCEALRGSPILYQFYHEDVTLGNSSAPSGGGSFNLSLTAHSGNSYCEANNG 373

QY 454 FGQRSKAVSLSTVP 469
 DB 374 LGAQCSEAVPVSISGP 389

RESULT 12

Q8N732 PRELIMINARY; PRT; 360 AA.

ID Q8N732 AC Q8N732
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE DJ80IG22.1 (Novel immunoglobulin domain protein similar to
 DE immunoglobulin receptors) (fragment).
 GN Name=dj80IG22.1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bagguley C.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL135929; CAB92753.1; -.
 DR HSP; P12319; I2Q.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig_3.
 DR SMART; SM00408; IGC2; 1.
 DR RECEPTOR; PSS0835; IG_LIKE; 4.
 KW RECEPTOR.
 FT NON_TER 1
 FT NON_TER 360
 SQ SEQUENCE 360 AA; 40724 MW; 7ACC2E7FA3256D62 CRC64;

Query Match 24.7%; Score 772; DB 2; Length 360;
 Best Local Similarity 46.1%; Pred. No. 1.7e-47;
 Matches 165; Conservative 49; Mismatches 138; Indels 6; Gaps 4;

QY 22 RPIIFLQPPVTTVQGERVLTCKGRRFFYSQTKWYHLYGKILRETPDNLLEQESG 81
 DB 4 KPVISVHPPTTFPKGERVLTLCNGFQFYATEKTVTHRRHWGKULTLTPGNTLVRESG 63

QY 82 EYRCQAGSPLSPVHLDFSSASLILOAPLSVEGDSVVLRCRAKAEVTLNNTIYK-NDN 140
 DB 64 LYRCQAGSPLSPVHLDFSSASLILOAPLSVEGDSVVLRCRAKAEVTLNNTIYK-NDN 123

QY 141 VLAFLNKRTPDHPHACLKNDGAYRCCTGYKESCCPVSSNTVKIQVQEPFTRPVLRASSFPQ 200
 DB 124 ILSISNKSMDULLIPQASSNNNGNYRCIGYDENDVFRSNPKIKIQELFPHPELKAATDSQ 183

QY 201 PISGNPVTLCETQLSLERSDVLRFRRFRDDQTLGLGWSLSPNQITAMSKDSGFWYCW 260
 DB 184 PTEGNSVNLSCETQLPERSDTPHFNFRRFDGEVILSDWSTYPELQLPTVWRENSGSWYC 243

QY 261 KAAATMHSVLSDSRSPWQVQ-IPASHPVLTLSPEKALNFEQTKVTLHCETQDSRLTRY 319
 DB 244 GAETVRGNIHKHSPLSIHVQIPVSGVLTETQPSGGQAVEGEMLVLCVSAEGTGDITF 303

QY 320 RFYHEGV--PLRHKSVCRCGASISFSLTTENSGNYCTADNGLGAKPKSKAVSLSVTV 375
 DB 304 SWHREDQBSLGRKTRSLRAELPAIROSHAGGYCTADNSYG--PVQSMVLNVTV 359

RESULT 13

Q8BJA5 PRELIMINARY; PRT; 508 AA.

ID Q8BJA5 AC Q8BJA5
 DT 01-MAR-2003 (T-EMBLrel. 23, Created)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Mus musculus activated spleen cDNA, RIKEN full-length enriched
 DE library, clone: F830015f10 product: weakly similar to SH2 DOMAIN-
 DE CONTAINING PHOSPHATASE ANCHOR PROTEIN 1C.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayaehizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayaehizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD; TISSUE=Activated spleen;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,
 RA Sumi N., Iehi Y., Nakamura S., Hazama M., Nishine T., Harada A.,

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RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [16]
RN SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Activated spleen;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK089756; BAC40954.1; -.
DR HSP; P12319; IP2Q.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00408; IgC2; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
SQ SEQUENCE 508 AA; 56795 MW; 27774A473BA9443F CRC64;

Query Match 22.2%; Score 692.5; DB 2; Length 508;
Best Local Similarity 40.9%; Pred. No. 1.5e-41;
Matches 160; Conservative 63; Mismatches 131; Indels 37; Gaps 6;

QY 105 LILQAPLSPVSGDVLRCRCAAEVTLNN-TIYKNDNVLAFLNKRDFHPIHACLKDNKA 163
DB 31 LVLOAPPVAFVFGDVSVLRCYAKGIEATLTFYKDGKALTLHPQSSELYIHANLKDNGO 90
QY 164 YRCTGYKESC--CPVSNTVKIQVEPFTPLVLRASFPQISGNPVLTCETQLSLERSD 221
DB 91 YKCTSKKWSFGSLYTSNTVRVQVELFPRPVLRRPSPHIDGSPVTLTCOTQLSAQKSD 150
QY 222 VPLRFRPRDQTLGLHSLSPNFOITAMWSKDSGFYKCAATWPHSVISDSRSPRQIQV 281
DB 151 ARLOPFCFRNLQLLGSGCSRSSEFHPAIMEESKRYQCKAETVNSQVRKQSTAFIPVQ 210
QY 282 IPASHPVLTLPGERALNPEGTGKVLTHCETQDSLTLYRFYHEGVP-----LRH 330
DB 211 RASARFQTHIPASKLVFEGQLLLNCSV-----KGVPGLKFSWYKMDLN 257
QY 331 KSVRCERGASISFSLTTN--SGNYCTADNGLGAKPSKAVSLSVTPVPSHPVLNLSSP 387
DB 258 KETKLKSNABFKISQVNIISDAGEYHREATNRRSFVSRAPFIIKVPVSPVLTSTG 317
QY 388 EDLIEGAKVTHLCEAQRGSLPILYQPHHDAALERSANSAGGVASISFSLTAHSGNYY 447
DB 318 KTOALEGDLMTLHCQSGSPCLLYEYFENVSLGNSILSGGAYFNFSMTERSGNYY 377
QY 448 CTADNGFGPQRSKAVSLSI-----TVPVS 471
DB 378 CTADNGLGACQCEAISRISIFDMTKNRSVPMA 408

RESULT 14
Q8NF56 PRELIMINARY; PRT; 437 AA.
AC Q8NF56;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE "A family of highly diverse human and mouse genes structurally links
DE leukocyte FcR, gp42 and PECAM-1.";
GN Name=FLJ00333;

OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK090423; BAC03404.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; Ig; 3.
DR PROSITE; PS00835; IG_LIKE; 3.
FT NON TER 1
FT SEQUENCE 437 AA; 46521 MW; F56DED36523E52CA CRC64;

Query Match 21.0%; Score 657.5; DB 2; Length 437;
Best Local Similarity 50.5%; Pred. No. 4.2e-39;
Matches 140; Conservative 29; Mismatches 101; Indels 7; Gaps 2;

QY 291 LSPKALNPEGTGK-----VTLHCETQDSLTLYRFYHEGVPLRHKSVCERGSISFS 344
DB 24 LAPSPSGGFPQAQVVDLLELHCEAPRGSPPLLYWYFHYEDVTLGSSSAPSGCEASFNL 83
QY 345 LTTNSNGNYCTADNGLGAKPSKAVSLSVTPVPSHPVLNLSSPEDLIFEGAKVTLHCEAQ 404
DB 84 LTAHSGNYSCEANGLVAQHSDTISLSVTPVPSRPLTPRAPRAQAVVDLLELHCEAL 143
QY 405 RGSPLILYQPHHDAALERSANSAGGVASISFSLTAHSGNYYCTADNGLGPGQSRKAVSL 464
DB 144 RGSPLILYWYFHYEDVTLGKISAPSGGASFNLSLTTEHSGIYSCDANGLEAQRSEWVL 203
QY 465 SITVPVPSHPVLTLSSAEALTFEGATVTLHCEVQSGSPQILYQPHHDMPLVSSSTPSVGR 524
DB 204 KAVPVPSPVLTLPAPGTHAAVGLLELHCEALRGSPLILYRFHFEDVTLGNRSSPS-GG 262
QY 525 VSFSPSLTEHSGNYYCTADNGLGPGQSRSEVSLFVTG 561
DB 263 ASLNLSLTAHSGNYSCEADNGLGAQRSEVTLVITG 299

RESULT 15
Q9EQY5 PRELIMINARY; PRT; 509 AA.
AC Q9EQY5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MMAN-g protein precursor (iFGP2) (Mus musculus adult male diencephalon
DE cDNA, RIKEN full-length enriched library, clone:9330158F12
DE product:macrophage scavenger receptor 2, full insert sequence) (Mus
DE musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:2810439C17 product:macrophage scavenger
DE receptor 2, full insert sequence).
DE Name=Msr2; Synonyms=MMAN-g;
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RA Yoshimoto M., Matsumoto K., Ukai Y., Kitamura K.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX MEDLINE=22033006; PubMed=12037601; DOI=10.1007/s00251-002-0436-x;
RA Guselnikov S.V., Ershova S.A., Mechetina L.V., Najakshin A.M.,
RA Volkova O.Y., Alabyev B.Y., Taranin A.V.;
RT "A family of highly diverse human and mouse genes structurally links
RT leukocyte FcR, gp42 and PECAM-1.";
GN Name=FLJ00333;

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Immunogenetics 54:87-95(2002).

[3] SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J; TISSUE=Diencephalon, and Whole body;
 RX MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).

[4] SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J; TISSUE=Diencephalon, and Whole body;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).

[5] SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J; TISSUE=Diencephalon, and Whole body;
 RX The FANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).

[6] SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J; TISSUE=Diencephalon, and Whole body;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).

[7] SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J; TISSUE=Diencephalon, and Whole body;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao K., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).

[8] SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RX Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanganaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Saeki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

[9] SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J; TISSUE=Whole body;
 RX Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanganaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

Tejima Y., Toya T., Yamamura T., Yamanaka I., Yasunishi A.,
 Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB028174; BAB18569.1; -;
 DR EMBL; AF329486; AAL23896.1; -;
 DR EMBL; AK034125; BAC28595.1; -;
 DR EMBL; AK076123; BAC36201.1; -;
 DR HSP; Q08380; IBY2.
 DR MGD; MGI:1933397; Msr2.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR001190; Srcr_receptor.
 DR Pfam; PF00047; Ig; 3.
 DR Pfam; PF00530; SRCR; 1.
 DR PRINTS; PR00258; SPERACTRCPT.
 DR SMART; SM00408; IGC2; 2.
 DR SMART; SM00202; SR; 1.
 DR PROSITE; PSS00835; IG_LIKE; 4.
 DR PROSITE; PS00420; SRCR_1; 1.
 DR PROSITE; PS0287; SRCR_2; 1.
 KW Receptor; Signal.
 FT SIGNAL 1 17 Potential.
 FT CHAIN 18 509 Potential.
 SQ SEQUENCE 509 AA; 55787 MW; EAB422EAC1310ECC CRC64;

Query Match 19.2%; Score 600.5; DB 2; Length 509;
 Best Local Similarity 30.4%; Pred. No. 6.6e-35;
 Matches 147; Conservative 71; Mismatches 159; Indels 107; Gaps 8;

Qy 96 VHLDFSSASLILOAPLSVFEGDSVLRCAKAEVLTNTIYKDNV-LAFLNKRTDHPH 154
 Db 15 VQSDWLSISL----PHRSYEGDQVWISCTGNNGDIKRLKYFKDGYHIETYSASSYTR 70

Qy 155 HACLKONGAYRCTGYKESCCPV-----SSNTVKIQVQEPFTRPVLRASSFPIGNSPVTIT 210
 Db 71 NARGDSGSGSYCKADRRKFLFDITTEGTGKWLNVQELFPAPGLTASPLQFVEGSSVTL 130

Qy 211 CETQLSLERSDVLPRFRFRDQDTGLGWSLSPNFQITAMWSKDSGFYWCKAATMPSHVI 270
 Db 131 CNTWLPDSRATTQLRYSFFKDGHTLQSGWT-SSKFTISAKEDSGNYWCMTASRSVS 189

Qy 271 SDSPRSWIQVQ-IPASHPVLTLSPEKALNPEGTQVTLHCETQSDSLRFLRYFHEGVPLR 329
 Db 190 KQSHRSYIDVERIPVSQVMTMEIQPSRGWGEV----- 221

Qy 330 HKSVRCERGASISFSLTTEGSGNYCYCTADNGLGAKPSKAVSLVTPVPSHPVLNLSPPED 389
 Db 222 -----EP 223

Qy 390 LIPEGAKVLHCEAQRGSLPILYQFTHEDA--ALERRSANSAGGVAISFSLTASHSGNY 447
 Db 224 LVVEGEPVLVACSVAKGTGLITSWHQDTKESVGKKSQRVSQORVELEIPITRESHAGY 283

Qy 448 CTADNCGFGPORSKAVSLSTITVPVSHPVLTLSABALTFEGATVTLHCEVQSGSPQILYQF 507
 Db 284 CTADNNYGLIQSAIVNITVKIPVLNPLLSISVPGVLPFIDGVAELHCEKCRASPPVLYWF 343

Qy 508 YHEDMPLVSSSTPSGVRVSFSLTSGHSGNYCYCTADNCGEPQSRSEVVSFLVTKCWLVA 567
 Db 344 YHENITLANTSAFPGKASFLSLTAGHSGNSYCEAENAWGTRKSEVVTILNVT----- 396

Qy 568 SKPP 571
 Db 397 -EPP 399

Search completed: May 4, 2005, 11:38:00
 Job time : 82.8488 secs

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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:20:49 ; Search time 125.902 Seconds
(without alignments)
3001.261 Million cell updates/sec

Title: US-09-724-254A-41

Perfect score: 5116

Sequence: 1 MLWLVILLVLPVSGQFART.....KVASTVPVSGSLFIASSAPHR 977

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5116	100.0	977	4	AAB82315 Human imm
2	5116	100.0	977	7	ADM35237 Human LY1
3	5104	99.8	977	6	ABP97215 Tumour-as
4	4486	87.7	875	8	ABM82476 Human dia
5	4253	83.1	837	8	ABM82477 Human dia
6	3923	76.7	759	4	AAB82313 Human imm
7	3923	76.7	759	7	ADM35235 Human LY1
8	2962	57.9	592	4	AAB82314 Human imm
9	2962	57.9	592	7	ADM35236 Human LY1
10	1559	30.5	707	7	ADM06089 Human pro
11	1559	30.5	734	4	AAB82316 Human imm
12	1559	30.5	734	7	ADM35238 Human LY1
13	1556.5	30.4	733	8	ADL06557 Human tum
14	1541.5	30.1	727	6	ABB84668 Human SEC
15	1538.5	30.1	750	8	ABM84916 Human dia
16	1520	29.7	717	7	ADF74337 Human FCR
17	1516	29.6	717	7	ADF74338 Human FCR
18	1411	27.6	582	6	ABU99155 Human hum
19	1411	27.6	582	8	ADM33875 Human NOV
20	1408.5	27.5	718	8	ABM84917 Human dia
21	1376	26.9	707	8	ABM84918 Human dia
22	1367.5	26.7	554	7	ADF74336 Extracell
23	1305.5	23.6	639	7	ADJ70604 Human hea
24	1185	23.2	655	8	ABM84920 Human dia
25	1137	22.2	268	7	ADE08350 Novel pro

26	1120	21.9	222	5	ABP69283 Human pol
27	1116.5	21.8	641	8	ABM84919 Human dia
28	1029	20.1	570	7	ADF74389 Murine FC
29	1024.5	20.0	470	7	ADL22727 Human dis
30	931.5	18.2	508	4	AAB82317 Human imm
31	931.5	18.2	508	7	ADM35239 Human LY1
32	931.5	18.2	508	7	ADM35264 Human LY1
33	931.5	18.2	508	8	ADF89715 Human can
34	931.5	18.2	508	8	ADL06539 Human tum
35	927.5	18.1	489	7	ADF74316 Human FCR
36	900	17.6	181	5	ABP51264 Human MDD
37	900	17.6	181	5	ABP51409 Human MDD
38	889	17.4	468	7	ADF74391 Extracell
39	884.5	17.3	327	5	ABP63021 Human pol
40	871.5	17.0	421	6	ABU99156 Novel hum
41	871.5	17.0	421	6	ABU99157 Novel hum
42	871.5	17.0	421	8	ADM93877 Human NOV
43	864.5	16.9	445	7	ADM35268 Human LY1
44	861	16.8	460	7	ADM35273 Human LY1
45	858.5	16.8	380	7	ADF74334 Extracell

ALIGNMENTS

RESULT 1		AAB82315		AAB82315 standard; protein; 977 AA.	
XX	AA	AAB82315	DT	23-JUL-2001 (first entry)	
XX	AA	AAB82315	DT	Human immunoglobulin receptor isoform IRTA2c.	
DE	DE	Human immunoglobulin receptor isoform IRTA2c.	Immunoglobulin superfamily receptor translocation associated; IRTA;		
KW	KW	IRTA2c; human; immunoglobulin receptor; FC receptor; melanoma; lymphoma;	myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.		
KW	KW	myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.	Homo sapiens.		
OS	OS	Homo sapiens.	Location/Qualifiers		
XX	XX	Key	1..15		
FH	FH	Peptide	/label= Signal_peptide		
FT	FT	Protein	16..977		
FT	FT	Protein	/label= Mature_protein		
FT	FT	Modified-site	132..134		
FT	FT	Modified-site	/note= "Asn is N-glycosylated"		
FT	FT	Modified-site	383..385		
FT	FT	Modified-site	/note= "Asn is N-glycosylated"		
FT	FT	Modified-site	621..623		
FT	FT	Modified-site	/note= "Asn is N-glycosylated"		
FT	FT	Modified-site	631..633		
FT	FT	Modified-site	/note= "Asn is N-glycosylated"		
FT	FT	Modified-site	714..716		
FT	FT	Modified-site	/note= "Asn is N-glycosylated"		
FT	FT	Modified-site	795..797		
FT	FT	Modified-site	/note= "Asn is N-glycosylated"		
FT	FT	Modified-site	806..808		
FT	FT	Modified-site	/note= "Asn is N-glycosylated"		
FT	FT	Modified-site	816..818		
FT	FT	Modified-site	/note= "Asn is N-glycosylated"		
FT	FT	Modified-site	843..845		
FT	FT	Modified-site	/note= "Asn is N-glycosylated"		
FT	FT	Domain	851..873		
FT	FT	Binding-site	/note= "transmembrane domain"		
FT	FT	Binding-site	899..902		
FT	FT	Binding-site	/note= "putative consensus Src-homology 2 (SH2) binding domain"		
FT	FT	Binding-site	924..927		
FT	FT	Binding-site	/note= "putative consensus Src-homology 2 (SH2) binding domain"		
FT	FT	Binding-site	954..957		

Thu May 5 15:11:00 2005

/note= "putative consensus Src-homology 2 (SH2) binding domain"

WO200138490-A2.

31-MAY-2001.

28-NOV-2000; 2000WO-US032403.

29-NOV-1999; 99US-0168151P.

(UYCO) UNIV COLUMBIA NEW YORK.

Dalla-Favera R;

WPI; 2001-355921/37.

N-PSDB; AAF30952.

New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor Translocation Associated proteins, used to treat B cell malignancies including lymphomas and multiple myeloma.

Claim 3; Fig 10B-1-18B-2; 72pp; English.

The present sequence is that of the novel human immunoglobulin receptor, immunoglobulin superfamily receptor translocation associated protein isoform 2c (IRTA2c), an Fc receptor involved in the pathogenesis of lymphoma and melanoma. Efforts to identify genes involved in chromosomal aberrations affecting band 1q21 in multiple myeloma and B cell lymphoma led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding members of a novel subfamily of related receptors within the immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82313 and AAB82314). IRTA2c is the longest isoform. It is a type I transmembrane glycoprotein. Each SH2 binding site agrees with the immune receptor tyrosine-based inhibition motif (ITIM) consensus and is encoded by a separate exon. The IRTA2 genes display a specific pattern of expression in mature B cells. IRTA2 is expressed in GC centrocytes and in perfollicular cells, which may include immunoblasts and memory cells. The invention provides IRTA nucleic acids and proteins, and antibodies directed to epitopes of IRTA proteins. Methods are claimed for: detecting a B cell malignancy comprising a 1q21 chromosomal rearrangement using a nucleic acid molecule that specifically hybridizes with a unique sequence of human IRTA1-5; and treating a subject having a B cell cancer by administering an anti-IRTA antibody or an antisense oligonucleotide that specifically hybridizes to IRTA mRNA so as to prevent overexpression of IRTA protein and hence to arrest cell growth or induce cell death of cancer cells expressing IRTA. The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma, multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse large cell lymphoma and follicular lymphoma. The B cell lymphoma is selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-Hodgkin's lymphoma

Sequence 977 AA;

Query Match 100.0%; Score 5116; DB 4; Length 977;
Best Local Similarity 100.0%; Pred. No. 2.le-315;
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLWVILLVAPVSGQFARTPIIFLOPPWTVFGSRVILTCCKGFRFYSPQKTWYHR 60
DB 1 MLLWVILLVAPVSGQFARTPIIFLOPPWTVFGSRVILTCCKGFRFYSPQKTWYHR 60
QY 61 YLQKEILRETPDNILEVQSGEYRCAQSGPLSSPVHLDFSSAILQAPLSVFEGDSV 120
DB 61 YLQKEILRETPDNILEVQSGEYRCAQSGPLSSPVHLDFSSAILQAPLSVFEGDSV 120
QY 121 LRCRAKEVTLNNTIYKNDVLAFLNKRDTDFHIFACLDKNGAYRCTGKSCCPVSNT 180
DB 121 LRCRAKEVTLNNTIYKNDVLAFLNKRDTDFHIFACLDKNGAYRCTGKSCCPVSNT 180
QY 181 VKIQVQEPFTRPVLRASSFQPISGNPVTLTCEITQSLERSDVPLRFRFRDDQTGLGWS 240

181 VKIQVQEPFTRPVLRASSFQPISGNPVTLTCEITQSLERSDVPLRFRFRDDQTGLGWS 240
QY 241 LSPNFQITAMWSKDSGFYWCKAATMPSHVISDSRSHIQVQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYWCKAATMPSHVISDSRSHIQVQIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTLHCEITQSDSLRTLYRFYHGVPLRHKSVCRCGASISFSLTTTNSGNYCYCTADNG 360
DB 301 GTKVTLHCEITQSDSLRTLYRFYHGVPLRHKSVCRCGASISFSLTTTNSGNYCYCTADNG 360
QY 361 LGAKPSKAVSLSVTVPVSHPVNLNLSPPDLIFEGAKVTLHCEAQSGSPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTVPVSHPVNLNLSPPDLIFEGAKVTLHCEAQSGSPILYQFHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFQPSKAVSLSVTVPVSHPVLTLSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFQPSKAVSLSVTVPVSHPVLTLSA 480
QY 481 EALTTFEGATVTLHCEVQSGPQILYQFYHEDMPLMSSSTPVSGRVSFSLTEGHSNYY 540
DB 481 EALTTFEGATVTLHCEVQSGPQILYQFYHEDMPLMSSSTPVSGRVSFSLTEGHSNYY 540
QY 541 CTADNGFGPQPSVNSLFTVTVPSRPILTLRVPRQAQVVDLLELHCEAPRGPSPILYWF 600
DB 541 CTADNGFGPQPSVNSLFTVTVPSRPILTLRVPRQAQVVDLLELHCEAPRGPSPILYWF 600
QY 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660
DB 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660
QY 661 LTFRAPRAQAVVGDLELHCEALRGSPILYWFYHEDVTLGKISAPSGGASFNLSLTTT 720
DB 661 LTFRAPRAQAVVGDLELHCEALRGSPILYWFYHEDVTLGKISAPSGGASFNLSLTTT 720
QY 721 HSGIYSCADNGLFAORSEMVTLKVAVPVSRPVLTLRPGTHAAVGDLELHCEALRGSP 780
DB 721 HSGIYSCADNGLFAORSEMVTLKVAVPVSRPVLTLRPGTHAAVGDLELHCEALRGSP 780
QY 781 LILYRFHEDVTLGNRSPSGGASLNLSTAHSNGNYSCEADNGLGAQRSETVLYITGL 840
DB 781 LILYRFHEDVTLGNRSPSGGASLNLSTAHSNGNYSCEADNGLGAQRSETVLYITGL 840
QY 841 TANRSGPATVAGGLLSIAGLAAGALLYCWLRSKAGRKPADPARSPSDSDSQEPTYH 900
DB 841 TANRSGPATVAGGLLSIAGLAAGALLYCWLRSKAGRKPADPARSPSDSDSQEPTYH 900
QY 901 NYPAMEELQPVVYTNANPRGENVYSEVRIOEKKKHAVASDPHRLNKGSPILYSEKVA 960
DB 901 NYPAMEELQPVVYTNANPRGENVYSEVRIOEKKKHAVASDPHRLNKGSPILYSEKVA 960
QY 961 STPVSGSLFLASSAPHR 977
DB 961 STPVSGSLFLASSAPHR 977

RESULT 2
ADM35237
ID . ADM35237 standard; protein; 977 AA.
XX
AC ADM35237;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human LY148P cancer related protein for cancer detection method.
XX
KW cytostatic; T-cell vaccine; detection; cancer;
KW chronic lymphocytic leukemia.
XX
OS Homo sapiens.
XX
FN WO2003077836-A2.
XX
PD 25-SEP-2003.

QY	721	HSGIYSCDADNGLEAQRSEMTTLKVAVPVSRPVLTLRAPGTHAAVGDILLEHCEALRGSP	780
DB	721	HSGIYSCDADNGPEAQRSEMTTLKVAVPVSRPVLTLRAPGTHAAVGDILLEHCEALRGSP	780
QY	781	LILYFFHHEDVTILGNRSPSGGASLNLSLTAESHGNYSCDADNGLGAORSETVTLITGL	840
DB	781	LILYFFHHEDVTILGNRSPSGGASLNLSLTAESHGNYSCDADNGLGAORSETVTLITGL	840
QY	841	TANRSGPATGVAGGLISIAAGALLLCWLSRKAGRKPASDPARSPDSOSPEPTH	900
DB	841	TANRSGPATGVAGGLISIAAGALLLCWLSRKAGRKPASDPARSPDSOSPEPTH	900
QY	901	NVPAMEELQPVTYNANPRGENVVYSFVRILIOEKKHAVASDPHLRNKGSPIIYSEVKVA	960
DB	901	NVPAMEELQPVTYNANPRGENVVYSFVRILIOEKKHAVASDPHLRNKGSPIIYSEVKVA	960
QY	961	STPVSGSLFLASSAPHR	977
DB	961	STPVSGSLFLASSAPHR	977
RESULT	4		
ID	ABM82476		
ID	ABM82476	standard; protein; 875 AA.	
XX	AC	ABM82476;	
XX	AC		
XX	DT	18-NOV-2004 (first entry)	
XX	DE	Human diagnostic and therapeutic pprotein SEQ ID NO:2725.	
XX	DE	gene therapy; human diagnostic and therapeutic polynucleotide; dithp.	
KW	XX		
XX	OS	Homo sapiens.	
XX	XX		
XX	PN	WO2004023973-A2.	
XX	PD	25-MAR-2004.	
XX	PP	12-SEP-2003; 2003WO-US028227.	
XX	XX		
XX	PR	12-SEP-2002; 2002US-0410259P.	
XX	PR	12-SEP-2002; 2002US-0410259P.	
XX	PA	(INCY-) INCYTE CORP.	
XX	PI	Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;	
PI	PI	Harthorne TA, Suchorski MT, Altus CM, Pitts SJ, Elder LV;	
PI	PI	Mooney EM, Delegeane AM, Fanser IS, Banville SC, Reddy TP;	
PI	PI	Stevens KA, Blanchard JL, Panux SR, Wang X, Au AP, Gerstin EH;	
PI	PI	Peralca CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;	
PI	PI	Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtson ES;	
PI	PI	Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;	
PI	PI	Patory S, Shi X, Suarez CJ;	
XX	XX		
DR	DR	WPI; 2004-329368/30.	
DR	DR	N-P5DB; ACN41128.	
XX	XX		
PT	PT	New diagnostic and therapeutic polynucleotides and polypeptides, useful	
PT	PT	in diagnosing a condition, disease or disorder associated with human	
PT	PT	molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or	
PT	PT	in gene mapping.	
XX	XX		
PS	PS	Claim 27; Page; 190pp; English.	
XX	XX		
CC	CC	The invention relates to novel diagnostic and therapeutic polynucleotides	
CC	CC	selected from one of the 2722 sequences defined in the specification. A	
CC	CC	polynucleotide of the invention may have a use in gene therapy. The human	
CC	CC	diagnostic and therapeutic polynucleotides (dithp) or polypeptides may b	
CC	CC	used to diagnose a particular condition, disease or disorder associated	
CC	CC	with human molecules, e.g. cell proliferative disorders,	
CC	CC	autoimmune/inflammatory disorder, developmental disorder, endocrine	
CC	CC	disorder, neurological disorders, gastrointestinal disorders, or	

CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 875 AA;

Query Match 87.78; Score 4486; DB 8; Length 875;
Best Local Similarity 88.83; Pred. No. 1.6e-275;
Matches 868; Conservative 4; Mismatches 2; Indels 104; Gaps 2;

Qy 1 MLLWVILLVLPVSGQPARTPRPIIFLOPPWTTFVQGERVTLCKGPRFYSPQTKWYHR 60
Db 1 MLLWVILLVLPVSGQPARTPRPIIFLOPPWTTFVQGERVTLCKGPRFYSPQTKWYHR 60
Qy 61 YLGEILRETPDNILEVOESGEYRCQAGSPLSPVHLDFSSASLILQAPLSVFEGBSVV 120
Db 61 YLGEILRETPDNILEVOESGEYRCQAGSPLSPVHLDFSSASLILQAPLSVFEGBSVV 120
Qy 121 LRCRAKAEVTLNNTIYKNDVNLAFNLKRTDFPHIACLKONGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDVNLAFNLKRTDFPHIACLKONGAYRCTGYKESCCPVSSNT 180
Qy 181 VKIQVQEPFTRPVLRASSFOPISGNPVTLCETQLSLERSDVLPRFRFRDDOTLGLGWS 240
Db 181 VKIQVQEPFTRPVLRASSFOPISGNPVTLCETQLSLERSDVLPRFRFRDDOTLGLGWS 240
Qy 241 LSPNQITAMWSKDSGYWCKAATMPHSVTSIPRSWIVQIOPASHPVLTLSPKALNPE 300
Db 241 LSPNQITAMWSKDSGYWCKAATMPYSVTSIPRSWIVQIOPASHPVLTLSPKALNPE 300
Qy 301 GTKVTLCETQDSRLTYFYHEGVPLRHKSVRCERGASISLTTENGNYCYTADNG 360
Db 301 GTKVTLCETQDSRLTYFYHEGVPLRHKSVRCERGASISLTTENGNYCYTADNG 360
Qy 361 LGAKPSKAVSLVTPVSHVPLNLSPEDILFEGAKVTLHCEAQRGSLPLIYQFHEDAA 420
Db 361 LGAKPSKAVSLVTPVSHVPLNLSPEDILFEGAKVTLHCEAQRGSLPLIYQFHEDAA 420
Qy 421 LERRSANSAGVAISFSLTAHSGNYCYTADNGFGPQRSKAVSLITVPVSHPVLTLSSA 480
Db 421 LERRSANSAGVAISFSLTAHSGNYCYTADNGFGPQRSKAVSLITVPVSHPVLTLSSA 480
Qy 481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVFSFSLTGHSGNY 540
Db 481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVFSFSLTGHSGNY 540
Qy 541 CTADNGFGPQRSEVSLF-VTVPSRPIILTRVPRAQAVVDLLELHCEAPRGPPILYW 599
Db 541 CTADNGFGPQRSEVSLFVSFVSVPSPILTRVPRAQAVVDLLELHCEAPRGPPILYW 600
Qy 600 FYHEDVTLGSSAPSGEASFNLSLTAHSGNYSCEANGLVAHQSDTISLSVIVPSRP 659
Db 601 FYHEDVTLGSSAPSGEASFNLSLTAHSGNYSCEANGLVAHQSDTISLSVIVPSRP 660
Qy 660 ILTFRAPRAQAVVDLLELHCEALRGSSPLIYFYHEDVTGKISAPSGGGASFNLSLT 719
Db 661 ILTFR----- 665
Qy 720 EHSGLYSCDANGLEAQRSEMTLKVAVPVRPVLTLRAPGTHAAVGDLLLELHCEALRG 779
Db 666 -----LLELHCEALRG 677
Qy 780 PLILYRFFHEDVTIGNRSSPGGASLNLSTAEHSGNYSCEADNGLGAQRSEVTLYITG 839
Db 678 PLILYRFFHEDVTIGNRSSPGGASLNLSTAEHSGNYSCEADNGLGAQRSEVTLYITG 737
Qy 840 LTANRSGPFATGVAGGLLSTAGLAAGALLYCWLRSKAGKPKASDPARSPSDSDSQBPTY 899
Db 840 LTANRSGPFATGVAGGLLSTAGLAAGALLYCWLRSKAGKPKASDPARSPSDSDSQBPTY 899

Db 738 LTANRSGPFATGVAGGLLSTAGLAAGALLYCWLRSKAGKPKASDPARSPSDSDSQBPTY 797
Qy 900 HNPVAMEELQPVVTNANPRGENVYSEVRIIQEKKKHAVASDPRHLRNKSGSPIIYSEVKV 959
Db 798 HNPVAMEELQPVVTNANPRGENVYSEVRIIQEKKKHAVASDPRHLRNKSGSPIIYSEVKV 857
Qy 960 ASTPVGSLFLASSAPHR 977
Db 858 ASTPVGSLFLASSAPHR 875

RESULT 5
ABM82477
ID ABM82477 standard; protein; 837 AA.
XX
AC ABM82477;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2726.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
XX
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Deleane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
PI Paralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve JL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtson ES;
PI Xu Y, Kwong M, Pollicky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Fatyry S, Shi X, Suarez CJ;
XX
DR WPI: 2004-329368/30.
DR N-PSDB; ACN41129.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 837 AA;

Query Match		83.1%	Score 4253;	DB 8;	Length 837;
Best Local Similarity		84.8%	Pred. No. 8.6e-261;		
Matches 829;		Conservative 4;	Mismatches 3;	Indels 142;	Gaps 3;
Qy	1	MLLWVLLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSPOKTKVHR	60		
Db	1	MLLWVLLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSPOKTKVHR	60		
Qy	61	YLKELIRETPNIILEVESGEYRCQAGSPVHLDFSSASLILQAPLSVPEGDSV	120		
Db	61	YLKELIRETPNIILEVESGEYRCQAGSPVHLDFSSASLILQAPLSVPEGDSV	120		
Qy	121	LRCKAEVTLNNTIYKNDNVLAFLNKRTPHIFACIKDNGAYRCTGYKSCCPVSSNT	180		
Db	121	LRCKAEVTLNNTIYKNDNVLAFLNKRTPHIFACIKDNGAYRCTGYKSCCPVSSNT	180		
Qy	181	VKIQOEPTRPVLRASSQPIISGNPVTLCETOLSLERSDVPFRFRDDOTLGLGWS	240		
Db	181	VKIQOEPTRPVLRASSQPIISGNPVTLCETOLSLERSDVPFRFRDDOTLGLGWS	240		
Qy	241	LSPNFOITAMWSDGQFYKCKAATPHSVISDPSRWIQVQIPASHPVLTLSPEKALNFE	300		
Db	241	LSPNFOITAMWSDGQFYKCKAATPHSVISDPSRWIQVQIPASHPVLTLSPEKALNFE	300		
Qy	301	GKVTLCETQEDSLRTLYRFYHEGVPLRHKSVRCERGASISFSLTTENSGNYCTADNG	360		
Db	301	GKVTLCETQEDSLRTLYRFYHEGVPLRHKSVRCERGASISFSLTTENSGNYCTADNG	360		
Qy	361	LGAKPSKAVSLSVTVSPHVLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA	420		
Db	361	LGAKPSKAVSLSVTVSPHVLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA	420		
Qy	421	LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRKAVSLSTVTVSPHVLTLSSA	480		
Db	421	LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRKAVSLSTVTVSPHVLTLSSA	480		
Qy	481	EALTPEGATVTLCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGY	540		
Db	481	EALTPEGATVTLCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGY	540		
Qy	541	CTADNGFGPQRSEVVSUFL-VTVPSVRPILTRVPRAQVVGDLLELHCEAPRGSPILY	599		
Db	541	CTADNGFGPQRSEVVSUFL-VTVPSVRPILTRVPRAQVVGDLLELHCEAPRGSPILY	599		
Qy	600	FYHEDVTLGSSAPSGGEAFNLSTAEHSGNYSCAANGLVAQSDTISLTVIVPSRP	659		
Db	600	FYHEDVTLGSSAPSGGEAFNLSTAEHSGNYSCAANGLVAQSDTISLTVIVPSRP	659		
Qy	660	ILTRAPRAQVVGDLLELHCEALRGSSPILYFYHEDVTLGKISAPSGGASFNLSLT	719		
Db	660	ILTRAPRAQVVGDLLELHCEALRGSSPILYFYHEDVTLGKISAPSGGASFNLSLT	719		
Qy	720	EHSGIYSCADNGLEAQRSEMTLVKAVPVSRPVLTRAPGTHAAVGDLELHCEALRG	779		
Db	720	EHSGIYSCADNGLEAQRSEMTLVKAVPVSRPVLTRAPGTHAAVGDLELHCEALRG	779		
Qy	780	PLIILYRPFHEDVTLGNRSSPGGASLNLSTAEHSGNYSCAANGLVAQSDTISLTVITG	839		
Db	780	PLIILYRPFHEDVTLGNRSSPGGASLNLSTAEHSGNYSCAANGLVAQSDTISLTVITG	839		
Qy	840	LTANRSGPFGATGVAGGLLSIAGLAAGALLLYCMLSRKAGRPASDPARSFSDSQBPT	899		
Db	840	LTANRSGPFGATGVAGGLLSIAGLAAGALLLYCMLSRKAGRPASDPARSFSDSQBPT	899		
Qy	900	HNPVAMELOPQVYTNANRGENVYSEVR11QEKKKHVASDPHRLNKGSPILYSEVK	959		
Db	900	HNPVAMELOPQVYTNANRGENVYSEVR11QEKKKHVASDPHRLNKGSPILYSEVK	959		
Qy	960	ASTPVSGSLFLASSAPHR 977			
Db	960	ASTPVSGSLFLASSAPHR 977			
Qy	820	ASTPVSGSLFLASSAPHR 837			
Db	820	ASTPVSGSLFLASSAPHR 837			

RESULT 6
AAB82313
ID AAB82313 standard; protein; 759 AA.
XX
AC AAB82313;
XX
23-JUL-2001 (first entry)
XX
Human immunoglobulin receptor isoform IRTA2a.
XX
Immunoglobulin superfamily receptor translocation associated; IRTA;
KW IRTA2a; human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma;
KW myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.
XX
Homo sapiens.
XX
Key Location/Qualifiers
Peptide 1..15
Protein 16..759
/label= Signal_peptide
/label= Mature_protein
Modified-site 132..134
/note= "Asn is N-glycosylated"
Modified-site 383..385
/note= "Asn is N-glycosylated"
Modified-site 621..623
/note= "Asn is N-glycosylated"
Modified-site 631..633
/note= "Asn is N-glycosylated"
Modified-site 714..716
/note= "Asn is N-glycosylated"
XX
WO200138490-A2.
XX
31-MAY-2001.
XX
28-NOV-2000; 2000WO-US032403.
XX
29-NOV-1999; 99US-0168151P.
XX
(UYCO) UNIV COLUMBIA NEW YORK.
XX
Dalla-Favera R;
XX
WPI; 2001-355921/37.
XX
N-PSDB; AAF30950.
XX
New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor
Translocation Associated proteins, used to treat B cell malignancies
including lymphomas and multiple myeloma.
XX
Claim 3; Fig 18B-1-18B-2; 72pp; English.
XX
The present sequence is that of the novel human immunoglobulin receptor,
immunoglobulin superfamily receptor translocation associated protein
isoform 2a (IRTA2a), an Fc receptor involved in the pathogenesis of
lymphoma and melanoma. Efforts to identify genes involved in chromosomal
aberrations affecting band 1q21 in multiple myeloma and B cell lymphoma
led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding
members of a novel subfamily of related receptors within the
immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA
isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82314 and AAB82315).
IRTA2a is a 759 amino acid secreted glycoprotein with 8 Ig-type domains
followed by a unique C-terminus. IRTA2b diverges from IRTA2a at residue
560, extending for a further 32 residues. IRTA2c diverges from IRTA2a at
residue 746 and extends for a further 231 residues. The IRTA genes
display a specific pattern of expression in mature B cells. IRTA2 is
expressed in GC centrocytes and in perifollicular cells, which may
include immunoblasts and memory cells. The invention provides IRTA
nucleic acids and proteins, and antibodies directed to an epitope of an
IRTA protein. Methods are claimed for: detecting a B cell malignancy
comprising a 1q21 chromosomal rearrangement using a nucleic acid molecule

CC that specifically hybridises with a unique sequence of human IRTA1-5; and
CC treating a subject having a B cell cancer by administering an anti-IRTA
CC antibody or an antisense oligonucleotide that specifically hybridises to
CC IRTA mRNA so as to prevent overexpression of IRTA protein and hence to
CC arrest cell growth or induce cell death of cancer cells expressing IRTA.
CC The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma,
CC multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse
CC large cell lymphoma and follicular lymphoma. The B cell lymphoma is
CC selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-
CC Hodgkin's lymphoma
XX
SQ Sequence 759 AA;

Query Match 76.7%; Score 3923; DB 4; Length 759;
Best Local Similarity 100.0%; Pred. No. 6.3e-240;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVLTCKGRFYSPQTKWYHR 60
Db |||||
QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVLTCKGRFYSPQTKWYHR 60
Db |||||
QY 61 YLGEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFFSSASLILOAPLSVFEQDSVV 120
Db |||||
QY 61 YLGEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFFSSASLILOAPLSVFEQDSVV 120
Db |||||
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKDNAGYRCTGYKESCCPVSSNT 180
Db |||||
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKDNAGYRCTGYKESCCPVSSNT 180
Db |||||
QY 181 VKIQVEPPTRPVLRASSFQPIISGNPVTITCETQSLERSDVLPRFRDQDTLGLWS 240
Db |||||
QY 181 VKIQVEPPTRPVLRASSFQPIISGNPVTITCETQSLERSDVLPRFRDQDTLGLWS 240
Db |||||
QY 241 LSPNFOITAMWSKDSGYWCKAATPHSVISDPSRWIOVQIPASHPVLTLSPEKALNFE 300
Db |||||
QY 241 LSPNFOITAMWSKDSGYWCKAATPHSVISDPSRWIOVQIPASHPVLTLSPEKALNFE 300
Db |||||
QY 301 GTKVTLHCETQEDSLRTLYFYHEGVPLRHKSVCRCGASISFSLTTNSGNYCYCTADNG 360
Db |||||
QY 301 GTKVTLHCETQEDSLRTLYFYHEGVPLRHKSVCRCGASISFSLTTNSGNYCYCTADNG 360
Db |||||
QY 361 LGAKPSKAVSLSTVTVSHVPLNLSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Db |||||
QY 361 LGAKPSKAVSLSTVTVSHVPLNLSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Db |||||
QY 421 LERRSANSAGGVAISFSLTAHSGNYCYCTADNGFGPQRSKAVSLSTVTVSHVPLTSSA 480
Db |||||
QY 421 LERRSANSAGGVAISFSLTAHSGNYCYCTADNGFGPQRSKAVSLSTVTVSHVPLTSSA 480
Db |||||
QY 481 EALTFFGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
Db |||||
QY 481 EALTFFGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
Db |||||
QY 541 CTADNGFGPQRSVSLFVTVPSRPTLTLVRPRAQAVGDLLELHCEAPRGSPPILYWF 600
Db |||||
QY 541 CTADNGFGPQRSVSLFVTVPSRPTLTLVRPRAQAVGDLLELHCEAPRGSPPILYWF 600
Db |||||
QY 601 YHEDVTLGSSSAPSGGEASFNLSLTAEHSGNYSCAANNGLVAQSDTISLSVTVPSRPI 660
Db |||||
QY 601 YHEDVTLGSSSAPSGGEASFNLSLTAEHSGNYSCAANNGLVAQSDTISLSVTVPSRPI 660
Db |||||
QY 661 LTFRAPRAQAVGDLLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720
Db |||||
QY 661 LTFRAPRAQAVGDLLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720
Db |||||
QY 721 HSGIYSCEADNGLEAQRSEMTLKVA 746
Db |||||
QY 721 HSGIYSCEADNGLEAQRSEMTLKVA 746
Db |||||

RESULT 7
ADM35235
ID ADM35235 standard; protein; 759 AA.

XX
AC ADM35235;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human LY1448P cancer related protein for cancer detection method.
XX
KW cytostatic; T-cell vaccine; detection; cancer;
KW chronic lymphocytic leukemia.
XX
OS Homo sapiens.
XX
FN WO2003077836-A2.
XX
PD 25-SEP-2003.
XX
PF 06-NOV-2002; 2002WO-US035728.
XX
PR 06-NOV-2001; 2001US-00040862.
PR 23-MAY-2002; 2002US-00154884.
XX
PA (CORI-) CORIXA CORP.
XX
PI Gaiger A, Algate PA, Mannion J, Retter M;
XX
DR WPI; 2003-756941/71.
XX
PT Detecting cancer in a patient comprises contacting a biological sample
PT from the patient with a binding agent that binds to a cancer-associated
PT polypeptide and comparing the amount of polypeptide to a predetermined
PT cutoff value.
XX
PS Disclosure; SEQ ID NO 10460; 419pp; English.
XX
CC The invention relates to a method of detecting (M1) cancer in a patient
CC by: (i) contacting a biological sample from the patient with an agent
CC that binds to any of three polypeptides given in the specification; (ii)
CC detecting in a sample an amount of the peptide that binds to the binding
CC agent; and (iii) comparing the amount of polypeptide present in the
CC patient's sample to a predetermined cutoff value. The specification also
CC discloses a separate method for detecting (M2) cancer in a patient by a
CC method similar to M1, except that the detection agent is an
CC oligonucleotide that binds to any of three polynucleotides given in the
CC specification. M1 and M2 are useful for detecting the presence of cancer
CC in a patient, especially chronic lymphocytic leukemia. The applicants
CC have identified specific human polypeptides overexpressed in one or more
CC types of hematological malignancies. This sequence corresponds to a
CC protein used in the method of the invention.
XX
SQ Sequence 759 AA;
Query Match 76.7%; Score 3923; DB 7; Length 759;
Best Local Similarity 100.0%; Pred. No. 6.3e-240; Indels 0; Gaps 0;
Matches 746; Conservative 0; Mismatches 0;
QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVLTCKGRFYSPQTKWYHR 60
Db |||||
QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVLTCKGRFYSPQTKWYHR 60
Db |||||
QY 61 YLGEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFFSSASLILOAPLSVFEQDSVV 120
Db |||||
QY 61 YLGEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFFSSASLILOAPLSVFEQDSVV 120
Db |||||
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKDNAGYRCTGYKESCCPVSSNT 180
Db |||||
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKDNAGYRCTGYKESCCPVSSNT 180
Db |||||
QY 181 VKIQVEPPTRPVLRASSFQPIISGNPVTITCETQSLERSDVLPRFRDQDTLGLWS 240
Db |||||
QY 181 VKIQVEPPTRPVLRASSFQPIISGNPVTITCETQSLERSDVLPRFRDQDTLGLWS 240
Db |||||
QY 241 LSPNFOITAMWSKDSGYWCKAATPHSVISDPSRWIOVQIPASHPVLTLSPEKALNFE 300
Db |||||

DB 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSHVSDSPRSWIQVQIPASHVPLTSPKALNFE 300
QY 301 GTRKVTLHCETQDSRLTLYRFYHEGVPLRHKSVCRCERGASISFSLTTSNGNYCYTADNG 360
DB 301 GTRKVTLHCETQDSRLTLYRFYHEGVPLRHKSVCRCERGASISFSLTTSNGNYCYTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLNSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTPVSHPVNLNSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420
QY 421 LERRANSAGGVAISFSLTAHSGNYCYTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
DB 421 LERRANSAGGVAISFSLTAHSGNYCYTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
QY 481 EALTTEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPVSFSGSLTEGHSNGY 540
DB 481 EALTTEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPVSFSGSLTEGHSNGY 540
QY 541 CTADNGFGPQRSEVSLFVTPVSPRPILTLRVPRAQAVVGDLELHCEAPRGSPPILYWF 600
DB 541 CTADNGFGPQRSEVSLFVTPVSPRPILTLRVPRAQAVVGDLELHCEAPRGSPPILYWF 600
QY 601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPVSRI 660
DB 601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPVSRI 660
QY 661 LTFPRAPQAVVGDLELHCEALRGSSPILYFYHEDVTLGKISAPSGGASFNLSLTT 720
DB 661 LTFPRAPQAVVGDLELHCEALRGSSPILYFYHEDVTLGKISAPSGGASFNLSLTT 720
QY 721 HSGIYSCDADNGLEAQRSEWTLKVA 746
DB 721 HSGIYSCDADNGLEAQRSEWTLKVA 746

RESULT 8

AAB82314 ID AAB82314 standard; protein; 592 AA.
XX AAB82314;
AC AAB82314;
DT 23-JUL-2001 (first entry)
XX Human immunoglobulin receptor isoform IRTA2b.
DE Immunoglobulin superfamily receptor translocation associated; IRTA;
KW IRTA2b; human; immunoglobulin receptor; FC receptor; melanoma; lymphoma;
KW myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..15
FT /label= signal_peptide
FT Protein 16..592
FT /label= Mature_protein
FT Modified-site 132..134
FT /note= "Asn is N-glycosylated"
FT Modified-site 383..385
FT /note= "Asn is N-glycosylated"
XX WO200138490-A2.
FN
XX
XX 31-MAY-2001.
XX
XX 28-NOV-2000; 2000WO-US032403.
XX
XX 29-NOV-1999; 99US-0168151P.
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX Dalla-Favera R;
XX

WPI: 2001-355921/37.
N-PSDB; AAF30951.

New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor Translocation Associated proteins, used to treat B cell malignancies including lymphomas and multiple myeloma.

Claim 3; Fig 18B-1-18B-2; 72pp; English.

The present sequence is that of the novel human immunoglobulin receptor, immunoglobulin superfamily receptor translocation associated protein isoform 2b (IRTA2b), an FC receptor involved in the pathogenesis of lymphoma and melanoma. Efforts to identify genes involved in chromosomal aberrations affecting band 1q21 in multiple myeloma and B cell lymphoma led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding members of a novel subfamily of related receptors within the immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82314 and AAB82315). IRTA2b is a 592 amino acid glycoprotein, which diverges from IRTA2a at residue 560, extending for a further 32 residues, whose hydrophobicity suggest docking to the plasma membrane via a GPI anchor. The IRTA2 genes display a specific pattern of expression in mature B cells. IRTA2 is expressed in GC centrocytes and in perfollicular cells, which may include immunoblasts and memory cells. The invention provides IRTA nucleic acids and proteins, and antibodies directed to an epitope of an IRTA protein. Methods are claimed for: detecting a B cell malignancy comprising a 1q21 chromosomal rearrangement using a nucleic acid molecule that specifically hybridises with a unique sequence of human IRTA1-5; and treating a subject having a B cell cancer by administering an anti-IRTA antibody or an antisense oligonucleotide that specifically hybridises to IRTA mRNA so as to prevent overexpression of IRTA protein and hence to arrest cell growth or induce cell death of cancer cells expressing IRTA. The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma, multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse large cell lymphoma and follicular lymphoma. The B cell lymphoma is selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-Hodgkin's lymphoma

Sequence 592 AA;

Query Match 57.9%; Score 2962; DB 4; Length 592;
Best Local Similarity 98.6%; Pred. No. 3.8e-179;
Matches 564; Conservative 0; Mismatches 4; Indels 4; Gaps 1;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPQTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPQTKWYHR 60
QY 61 YLGKEILRETPDNIILEVQESGEYRCQAQSPVHLDFSSASLILOAPLSVEGDSVV 120
DB 61 YLGKEILRETPDNIILEVQESGEYRCQAQSPVHLDFSSASLILOAPLSVEGDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDPhiHACLKDNGAVRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDPhiHACLKDNGAVRCTGYKESCCPVSSNT 180
QY 181 VKIQVEPPTRPVLRASSFPQISGNPVTLCETQLSLERSDVPLFRFRDDQTGLGWS 240
DB 181 VKIQVEPPTRPVLRASSFPQISGNPVTLCETQLSLERSDVPLFRFRDDQTGLGWS 240
QY 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSHVSDSPRSWIQVQIPASHVPLTSPKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSHVSDSPRSWIQVQIPASHVPLTSPKALNFE 300
QY 301 GTRKVTLHCETQDSRLTLYRFYHEGVPLRHKSVCRCERGASISFSLTTSNGNYCYTADNG 360
DB 301 GTRKVTLHCETQDSRLTLYRFYHEGVPLRHKSVCRCERGASISFSLTTSNGNYCYTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLNSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTPVSHPVNLNSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420
QY 421 LERRANSAGGVAISFSLTAHSGNYCYTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480

Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
Qy 481 EALTFFEGATVTLHCEVQSGPQILYQFVHEDMPLWSSSTPSVGRVSFSLTEHSGNYY 540
Db 481 EALTFFEGATVTLHCEVQSGPQILYQFVHEDMPLWSSSTPSVGRVSFSLTEHSGNYY 540
Qy 541 CTADNGFGPQSRSEVSLFVT----VPVSRPIL 568
Db 541 CTADNGFGPQSRSEVSLFVTGKCWLASHPPL 572

RESULT 9

ADM35236
ID ADM35236 standard; protein; 592 AA.
XX AC ADM35236;
XX DT 03-JUN-2004 (first entry)
XX Human LY1448P cancer related protein for cancer detection method.
XX cytostatic; T-cell vaccine; detection; cancer;
XX chronic lymphocytic leukemia.
XX OS Homo sapiens.
XX PN W02003077836-A2.
XX PD 25-SEP-2003.
XX PF 06-NOV-2002; 2002WO-US035728.
XX PR 06-NOV-2001; 2001US-00040862.
XX PR 23-MAY-2002; 2002US-00154884.
XX PA (CORI-) CORIXA CORP.

XX Gaiger A, Algate PA, Mannion J, Retter M;
XX WPI; 2003-756941/71.
XX Detecting cancer in a patient comprises contacting a biological sample
PT from the patient with a binding agent that binds to a cancer-associated
PT polypeptide and comparing the amount of polypeptide to a predetermined
PT cutoff value.
XX Disclosure; SEQ ID NO 10461; 419pp; English.

XX The invention relates to a method of detecting (M1) cancer in a patient
CC by: (i) contacting a biological sample from the patient with an agent
CC that binds to any of three polypeptides given in the specification; (ii)
CC detecting in a sample an amount of the peptide that binds to the binding
CC agent; and (iii) comparing the amount of polypeptide present in the
CC patient's sample to a predetermined cutoff value. The specification also
CC discloses a separate method for detecting (M2) cancer in a patient by a
CC method similar to M1, except that the detection agent is an
CC oligonucleotide that binds to any of three polynucleotides given in the
CC specification. M1 and M2 are useful for detecting the presence of cancer
CC in a patient, especially chronic lymphocytic leukemia. The applicants
CC have identified specific human polypeptides overexpressed in one or more
CC types of hematological malignancies. This sequence corresponds to a
CC protein used in the method of the invention.

XX Sequence 592 AA;
Query Match 57.9%; Score 2962; DB 7; Length 592;
Best Local Similarity 98.6%; Pred. No. 3.8e-179;
Matches 564; Conservative 0; Mismatches 4; Indels 4; Gaps 1;

Qy 1 MLLWVILLVLPVSGQPARTPRPIIFLOPWTTFQGERVTLCKGPRFYSPOKTKWYHR 60
Db 1 MLLWVILLVLPVSGQPARTPRPIIFLOPWTTFQGERVTLCKGPRFYSPOKTKWYHR 60

Qy 61 YLKGKILRETPDNIQVQESGEYRCQAQGSPLSPVHLDFSSASLIIQAPLSVEGDSVV 120
Db 61 YLKGKILRETPDNIQVQESGEYRCQAQGSPLSPVHLDFSSASLIIQAPLSVEGDSVV 120
Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKONGAYRCTGYKSCCPVSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKONGAYRCTGYKSCCPVSNT 180
Qy 181 VKIQVQEPFTRPVLRASSFPISGNPVTLCETQLSLERSDVPLRFRFRDDQTLGLGWS 240
Db 181 VKIQVQEPFTRPVLRASSFPISGNPVTLCETQLSLERSDVPLRFRFRDDQTLGLGWS 240
Qy 241 LSPNQITAMWSKDSGFYWCKAATMPSHSVISDSPRSIIQVQIPASHPVLTLSPEKALNFE 300
Db 241 LSPNQITAMWSKDSGFYWCKAATMPSHSVISDSPRSIIQVQIPASHPVLTLSPEKALNFE 300
Qy 301 GTKVTLHCETOEDSLRTLYRFYHEGVPLRHSVRCERGASISFSLTTEHSGNYCTADNG 360
Db 301 GTKVTLHCETOEDSLRTLYRFYHEGVPLRHSVRCERGASISFSLTTEHSGNYCTADNG 360
Qy 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFFGAKVTLHCEAQSGSLPILYQFHHDDAA 420
Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFFGAKVTLHCEAQSGSLPILYQFHHDDAA 420
Qy 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
Qy 481 EALTFFEGATVTLHCEVQSGPQILYQFVHEDMPLWSSSTPSVGRVSFSLTEHSGNYY 540
Db 481 EALTFFEGATVTLHCEVQSGPQILYQFVHEDMPLWSSSTPSVGRVSFSLTEHSGNYY 540
Qy 541 CTADNGFGPQSRSEVSLFVT----VPVSRPIL 568
Db 541 CTADNGFGPQSRSEVSLFVTGKCWLASHPPL 572

RESULT 10

ADM06089
ID ADM06089 standard; protein; 707 AA.
XX AC ADM06089;
XX DT 20-MAY-2004 (first entry)
XX Human protein of the invention SEQ ID NO:4774.
XX human; gene therapy; diagnostic marker; pharmaceutical.
XX Homo sapiens.
XX EP1347046-A1.
XX PD 24-SEP-2003.
XX PF 12-APR-2002; 2002EP-00008400.
XX PR 22-MAR-2002; 2002JP-00137785.
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
XX Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
XX Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX WPI; 2003-723558/69.
XX N-PSDB; ADM03646.

XX New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.

Claim 1; SEQ ID NO 4774; 305pp; English.

The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a protein sequence of the invention.

Query Match 30.5%; Score 1559; DB 7; Length 707;
 Best Local Similarity 37.1%; Pred. No. 4.2e-90;
 Matches 364; Conservative 94; Mismatches 216; Indels 306; Gaps 13;

QY 1 MLLWVILLVAVSGOFARTPRPIIFLOPPPTVFOGERVLTLCGKGRFYSPO-KTKWYH 59
 DB 1 MLLWVILLVLTGREGSGVAPKAVILLNPPWSTAFKGEKVALICSSISHSLAQDQTYWH 60
 QY 60 RYLGEILRETNDNILEQSEGEYRCOAQSPSLSPVHLDFSSALILQAPLSVFEQDSV 119
 DB 61 ---DEKLLIKHDKI-QITEPGNYCKTRGSSLSDAVHFSPDWLILQALHPVFEQDNV 116
 QY 120 VLRCRAKAEVTLNNTYKNDVLAFLNKTDRPHIACLKONGAVRCCTGYKESC---CPV 176
 DB 117 ILRCOGKDNKNTKQVYKDGKQLPNSVNLKITYNSVSDNSKHYCTAYRKFYILDIEV 176
 QY 177 SSNTVIOQEPRTPLVRASSFOPTSGNPFVLTLCETQLSLERSDVPLRFRFFDDQTLG 236
 DB 177 TSPLNIQVQELFHLVPLRASSFTPIEGSPMTLTCTQLSPQRPDVQLQSLFRDSQTLG 236
 QY 237 LGMSLSPNFQITAMWSKDSGFYWCKAATNPHSVISDPSRWITQVQIPASHVPLTILSPEKA 296
 DB 237 LGMSRSPKLQIPAMWTEDESGSYCEVETVTHSIKRLSRQIRVQ----- 281
 QY 297 LNFEGYKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVRCERGASISFSLTTEGNSNYCT 356
 DB 282 ----- 281
 QY 357 ADNLGAKPSKAVSLSVTVPSHPVLNLSPEDLIFEGAKVTLHCEAQRGSLPILYQPHH 416
 DB 282 -----RVPVSNVNLEIRPTGQIIEGEMVVLICSAVQAGSGTFTVFSWHK 324
 QY 417 ED--AALERSANSAGGVAISFSLTAHSGNYCYCTADNGFGPQRSKAVSLSTIVPSHPV 474
 DB 325 EGRVRSLSGRKT-----QRSLLAELH-----V 345
 QY 475 LTLSSAELTFEGATVTLHCEVQRSPQILYQFYHEDMPLWSSSTPSVGRVSFSLFTEG 534
 DB 346 LTVKESDA----- 353
 QY 535 HSGNYCYCTANGFGPQRSEVSLFVTVPSRPILTILVRPAQAVVGDILLEHCEAPRGPSP 594
 DB 354 --GRYCAADNVHSPILSTWIRVTVRIPVSHPLTFRAPHTVVGDLLEHCESLURGSP 411
 QY 595 PILYWFYHEDVTLGSSAPSGGASPNLSLTAHSGNYSCYCAANNGLVAQHSITISLSVIV 654
 DB 412 PILYRFYHEDVTLGNSAPSGGASPNLSLTAHSGNYSCDADNGLGAQSHGVSLRVIV 471
 QY 655 PVSRLPILTFRAPAAQVVDLLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGASPN 714
 DB 472 PVSRLPILTRAPAAQVVDLLEHCEALRGSSPILYWFYHEDVTLGNISAHSGGASPN 531
 QY 715 LSLTTEHSGIYSCDADNGLAQRSEMVTLVAVVPSRPVLTFRAPGTHAAGVLDLLEHCE 774
 DB 532 LSLAT----- 536
 QY 775 ALRGSPILTYLRFYHEDVTLGNRSSPFGASINLSLTAHSGNYSCDADNGLGAQRSETVT 834


```
QY 120 VLRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACILKONGAYRCTGYKESC---CPV 176
Db 117 ILRCQKDNKNTKQVYKDGKQLPNSVNSLEKITVNSVRDMSKXCHTAYRKFYILDIEV 176
QY 177 SSNTVKIQVEEPFTPRVLRASSFQISGNPNVTLCTQSLERSDVPLRFRFRDDQTLG 236
Db 177 TSKPLNIQVQELFLHPVLRASSSTIEGSPMTLTCTQSPQRPVQVQFSLFRDSQTLG 236
QY 237 LGWSLSPNFQITAMWSKDSGFYWCXAAATMPHSVSDSPRSMTQVQIPASHPVLTLSPEKA 296
Db 237 LGWSRSPRLQIPAMWTEDSGSYWCEVETVTHSIKRSLSRQIRVQ-----281
QY 297 LNFEGTKVTLHCETQEDSLRTLRYFYHGVPLRHKSVCRCGASISFSLTENSNGNYCT 356
Db 282 -----281
QY 357 ADNLGAKPSKAVSLSVTVPVSHPVNLNLSPPEDLIFEGAKVTLHCEAQRGSLPIYQFHH 416
Db 282 -----RVPVSNVNLEIRPTGGQLIEGENMVILCSVAQSGTWTFSWHK 324
QY 417 ED--AALERRSANSAGGVAISFSLTAHSGNYCTADNGCFGORSKAVSLSVTVVSHPV 474
Db 325 EGRVSLGRKT-----ORSLLAEHL-----V 345
QY 475 LTLSSAEALTPEGATVTLHCEVORGSPQLIYQFYHEDMPLWSSSTPSVGRVSFSLTEG 534
Db 346 LIVKESDA-----353
QY 535 HSGNYCTADNGFGORSSEVSLFVTVVSRPILTLRVPRAQAVVGDLLLELHCEAPRSP 594
Db 354 --GRYCAADNVHSPILSVIRVTRIPVSHPEVLTFRAPRAHTVVGDLLELHCESLRGP 411
QY 595 PILYFYHEDVTLGSSAPSAGCEASPNLSLTAHSGNYSCNANGIQAQHSPTISLSTIV 654
Db 412 PILYFYHEDVTLGSSAPSAGGASPNLSLTAHSGNYSCDADNGLGAQHSVGLRVTV 471
QY 655 PVSRLPILTRAPRAQAVVGDLLLELHCEALRGSPILYFYHEDVTLGKISAPSGGASPN 714
Db 472 PVSRLPILTRAPCAQAVVGDLLLELHCESLRGSPILYFYHEDDTLGNISAHSGGASPN 531
QY 715 LSLTTHSGIYSCDADNGLEAQRSEMVLKAVPVSRPVLTLRAPGTHAAVGDLLLELHCE 774
Db 532 LSLTT-----536
QY 775 ALRGSPILYFYHEDVTLGNRSSPSGASLNLSTAEHSGNYSCDADNGLGAQRSETV 834
Db 537 -----EHSNGYSCDADNGLGAQHSKVTV 559
QY 835 LVITGLTANRSGPFATGVAGGLISTAGLAAGALLLYCWLRSRAGRKP-----881
Db 560 LNVGTGSRNRTGLTAAGITGLVLSILVLAALAAALLH--YARARRKPGGLSATGTSSHSP 616
QY 882 --ASDPARS-PSDSDSQEPTYNVPABELOPVYTNANRGENVYVSEIRIIOEKKKHAV 938
Db 617 SECQEPSSRPSRIDQEPETHSKPLAPMELEPMYSNVNFCDSNPITYSOWISQHTKNSA 676
QY 939 ASDPRLHNRKSGPIIYSEVK 958
Db 677 NCPMMQHEHEELTVLSELK 696
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RESULT 13

```
ADL06557
ID ADL06557 standard; protein; 733 AA.
XX
XX ADL06557;
XX
XX 20-MAY-2004 (first entry)
XX Human tumour-associated antigenic target (TAT) polypeptide #56.
XX Human; tumour-associated antigenic target; TAT; cell death; tumour;
KW cancer; cytostatic.
```

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XX Homo sapiens.
OS WO2004016225-A2.
XX
XX 26-FEB-2004.
XX
XX 19-AUG-2003; 2003WO-US025892.
XX
XX 19-AUG-2002; 2002US-0404809P.
XX 21-AUG-2002; 2002US-0405645P.
XX 23-SEP-2002; 2002US-0413192P.
XX 15-OCT-2002; 2002US-0419008P.
XX 15-NOV-2002; 2002US-0426847P.
XX 02-JUL-2003; 2003US-0484959P.
XX
XX (GETH ) GENENTECH INC.
PA
Desauvage FJ, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V;
PI Spencer SD, Wu TD, Zhang Z;
PI
XX
XX MPI; 2004-257144/24.
XX N-PSDB; ADL06478.
XX
XX New antibody that binds to a tumor-associated antigenic target (TAT)
PT polypeptide, useful for preparing a composition for diagnosing or
PT treating cancer.
PT
XX
XX Claim 2; SEQ ID NO 137; 319pp; English.
PS
XX
XX The present invention relates to the isolation of human tumour-associated
CC antigenic target (TAT) polynucleotide and polypeptide sequences. Also
CC disclosed is an antibody that binds to a TAT polypeptide. The antibody is
CC a monoclonal antibody, an antibody fragment, a chimeric antibody or a
CC humanised antibody. It is conjugated to a growth inhibitory agent. It is
CC produced in bacteria or in CHO cells and induces death of a cell to which
CC it binds. The antibody is useful for preparing a composition for
CC diagnosing or treating tumours and cancer. The present sequence
CC represents a human TAT polypeptide of the invention.
XX
XX Sequence 733 AA;
```

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Query Match 30.4%; Score 1556.5; DB 8; Length 733;
Best Local Similarity 37.0%; Pred. No. 6.4e-90;
Matches 363; Conservative 95; Mismatches 215; Indels 307; Gaps 13;
QY 1 MLLWLLVLAIPVSGQFARTPRPIIFLOPPPTVTFQGBRVTILCKGFRFYSQ-KTKVWH 59
Db 1 MLLWLLVLLITLTPGREQSGVAPKAVLLNPPNSTAFKGEKVALICSSISHSLAQGDYVWH 60
QY 60 RYLKKEILRETPDNTILEVQESGEYRCQAQGPLSPVHLDPSSASLILQAPLSVFEQDSV 119
Db 61 ---DEKLLIKHD--IQITEPGNYCKTRGSSLSDAHVFEFSPDWLILQALHPVEGDV 115
QY 120 VLRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACILKONGAYRCTGYKESC---CPV 176
Db 116 ILRCQKDNKNTKQVYKDGKQLPNSVNSLEKITVNSVRDMSKXCHTAYRKFYILDIEV 175
QY 177 SSNTVKIQVEEPFTPRVLRASSFQISGNPNVTLCTQSLERSDVPLRFRFRDDQTLG 236
Db 176 TSKPLNIQVQELFLHPVLRASSSTIEGSPMTLTCTQSPQRPVQVQFSLFRDSQTLG 235
QY 237 LGWSLSPNFQITAMWSKDSGFYWCXAAATMPHSVSDSPRSMTQVQIPASHPVLTLSPEKA 296
Db 236 LGWSRSPRLQIPAMWTEDSGSYWCEVETVTHSIKRSLSRQIRVQ-----280
QY 297 LNFEGTKVTLHCETQEDSLRTLRYFYHGVPLRHKSVCRCGASISFSLTENSNGNYCT 356
Db 281 -----280
QY 357 ADNLGAKPSKAVSLSVTVPVSHPVNLNLSPPEDLIFEGAKVTLHCEAQRGSLPIYQFHH 416
Db 281 -----RVPVSNVNLEIRPTGGQLIEGENMVILCSVAQSGTWTFSWHK 323
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QY 417 ED--AALERSANSAGGVAISFSLTAHSGNYCYTADNGFGPQRKAVSLISITVPVSHPV 474
D 324 EGRVRSIGRKT-
QY 475 LTLSSAALTFEGATVTLHCEVQRGSPQLLYQFYHEDWMLWSSSTPVGVRVSFSLTEG 534
D 345 LTVKESA-----
QY 535 HSGNYCYTADNGFGPQRSEVSVLFTVPVPRPILTLRVPRAQAVVGDLELHCEAPRGSP 594
D 353 --GRYYCAADNVHSPILSTWIRVTRIPVSHPVLTFRAPRAHTVVGDLLELHCESLRGSP 410
QY 595 PILYFWFHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCAANGLVAQHSDDTISLSVIV 654
D 411 PILYFWFHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCAANGLVAQHSDDTISLSVIV 470
QY 655 PVSRLPILTFRAPRAQAVVGDLELHCEALRGSSPILYFWFHEDVTLGKISAPSGGASFN 714
D 471 PVSRLPILTFRAPRAQAVVGDLELHCEALRGSSPILYFWFHEDVTLGKISAPSGGASFN 530
QY 715 LSLTTEHSGIYSCADNGLEAQRSEMTLKVAVPVSRLPILTFRAPGTHAAVGDLELHCE 774
D 531 LSLTT-----
QY 775 ALRGSPILYRFFHEDVTLGNRSPSGASINLSLTAHSGNYSCAANGLGQRSETV 834
D 536 -----EHSNGYSCAANGLGQAHSKVVT 558
QY 835 LYITGLTANRSGPATGVAGGLISLAGALLLYCWLRSKAGRP----- 881
D 559 LNVGTGRNRGTGAAGITGLVLSILVLAALH---YARARRKPGGLSATGTSSHSP 615
QY 882 --ASDPARS-PSDSOEPYTHNPVWEELQPVYTNANPRGENVYSEVRIIOEKKHAV 938
D 616 SEQEPSSPSRDPPEPTKSLAPMELEPMYSNVNPDSNPIYQINSIQHTKNSA 675
QY 939 ASDPRHLNRKSPISYSEVK 958
D 676 NCPMMHQHEELTVLYSELK 695

RESULT 14
ABB84668
ID ABB84668 standard; protein; 727 AA.
AC ABB84668;
XX
XX 11-FEB-2003 (first entry)
DE Human SECP-20 protein from clone 8039739CD1 SEQ ID 20.
XX
XX Secreted protein; SECP; human; antiarteriosclerotic; antiatherosclerotic;
KW hepatotropic; cytosolic; anti-HIV; antiallergic; antiasthmatic; cancer;
KW antianemic; antidiabetic; antiinflammatory; neuroprotective; antiulcer;
KW antirheumatic; antiarthritic; cardiac; hypotensive; gonadal dysgenesis;
KW vasotrophic; anticonvulsant; nootropic; immunosuppressive; pericarditis;
KW antiparkinsonian; ophthalmological; cell proliferative disorder;
KW arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; angina pectoris;
KW autoimmune disorder; AIDS; Crohn's disease; multiple sclerosis; epilepsy;
KW ulcerative colitis; cardiovascular disorder; myocardial infarction;
KW Raynaud's disease; myocardiitis; neurological disorder; cataract;
KW Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;
KW developmental disorder; Duchenne muscular dystrophy; antipsoriatic;
KW Becker muscular dystrophy; Cushing's syndrome.
XX
OS Homo sapiens.
XX
XX WO200279441-A2.
XX
XX 10-OCT-2002.
XX
XX 29-MAR-2002; 2002WO-US009820.
XX
PF
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XX
PR 30-MAR-2001; 2001US-0280527P.
PR 06-APR-2001; 2001US-0282112P.
PR 09-APR-2001; 2001US-0282702P.
PR 13-APR-2001; 2001US-0283855P.
PR 19-OCT-2001; 2001US-0343718P.
PR 07-DEC-2001; 2001US-0339236P.
PR 13-FEB-2002; 2002US-0357002P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Baughn MR, Burford N, Ding L, Duggan BM, Elliott VS, Forsythe IJ;
XX Gandhi AR, Gietzen KU, Griffin JA, He A, Honchell CD, Ison CH;
XX Lal PG, Lee EA, Lee S, Lu DAM, Mason PM, Sanjanwala MM;
XX Swarnakar A, Ramkumar J, Tang YT, Thangavelu K, Tran UK, Wallia NK;
XX Warren BA, Yao MG, Xu Y, Yue H;
XX
XX WPI; 2003-058429/05.
XX N-PSDB; ABS57564.
XX
XX Novel human secreted protein useful for treating, preventing or
XX diagnosing cancer, hepatitis, psoriasis, asthma, diabetes mellitus,
XX anemia, epilepsy, cataract, Alzheimer's disease.
XX
XX Claim 75; Page 165-166; 188pp; English.
XX
XX This invention describes novel secreted proteins (SECP) which have
XX antiarteriosclerotic, antiatherosclerotic, hepatotropic, cytosolic, anti
XX -HIV, antiallergic, antiasthmatic, antianemic, antidiabetic, anti
XX antiinflammatory, neuroprotective, antiulcer, antipsoriatic, vasotrophic,
XX antirheumatic, antiarthritic, cardiac, hypotensive, anticonvulsant,
XX nootropic, immunosuppressive, antiparkinsonian and ophthalmological
XX activity. The polynucleotides and polypeptides of the invention can be
XX used for diagnosing, treating or preventing cell proliferative disorder
XX e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, cancer,
XX autoimmune/inflammatory disorders e.g. acquired immunodeficiency syndrome
XX (AIDS), allergies, asthma, anaemia, diabetes mellitus, Crohn's disease,
XX multiple sclerosis, ulcerative colitis, psoriasis, rheumatoid arthritis,
XX etc; cardiovascular disorder e.g. myocardial infarction, angina pectoris,
XX hypertension, Raynaud's disease, myocardiitis, pericarditis, etc;
XX neurological disorders e.g. epilepsy, Huntington's disease, Parkinson's
XX disease, Alzheimer's disease, Creutzfeldt-Jakob disease, etc; and
XX developmental disorders e.g. Duchenne and Becker muscular dystrophy,
XX cataract, gonadal dysgenesis, Cushing's syndrome, etc. The products of
XX the invention can also be used for drug screening, proteome analysis,
XX microarrays creating knock-in humanised animals or transgenic animals to
XX model human diseases, in somatic or germline gene therapy, to generate a
XX transcript image of a tissue or cell type, for detecting differences in
XX the chromosomal location due to translocation, inversion, etc., among
XX normal, carrier or affected individuals, and as hybridization probes for
XX mapping naturally occurring genomic sequences. ABB84649-ABB84673
XX represent secreted proteins encoded by the cDNA's shown in ABB57545-
XX ABB57569, described in the disclosure of the invention
XX
XX Sequence 727 AA;
XX
XX Query Match 30.1%; Score 1541.5; DB 6; Length 727;
XX Best Local Similarity 36.9%; Pred. No. 5.7e-89;
XX Matches 362; Conservative 94; Mismatches 211; Indels 313; Gaps 14;
XX
XX QY 1 MLLWLVLLVAPVSGQFARTPRPIIFLQPPWTVFQGERVLTCKGFRFYSPO-KTKWYH 59
XX Db 1 MLLWLVLLVLRV-----APKAVLLNPNPWSAFKGEKVALICSSISHSLAQDVTWYH 53
XX
XX QY 60 RYLGKILRETPDNILEVQESGYRQAOQSPSSPVLHDFSSASILQAPLSPVFGDSV 119
XX Db 54 ---DEKLLIKKHDKI-QITEPGNYQCKTRGSSLSDAHVFEFSPDLILQALHPVFGDNV 109
XX
XX QY 120 VLRCKRAEVTLLNNTIYKNDNLVLAFLNKRDTFHI PHACLKNDGAYRCTGYKESC---CPV 176
XX Db 110 ILRCQCKDNKNTQKQVYKDGKQLPNSYNLEKIVTSVSRDNRKYNHCTAYRKFYLDIEV 169
XX
XX QY 177 SSNTVKIQOEPTFRPVLRASSFPQISGNPVTLTCTQLSLERSDVLPRFRFRDDQTLG 236
```

Db 170 TSKPLNIQVQELFLHPVLRASSTIEGSPMLTCTQSLSPQRPVQLOFSLFRDSTLIG 229
QY 237 LGWSLSPNFQITAMWSKDSGFYCKAAATPHSVISDSRSPWQIQVPIPAHPVLTLSPEKA 296
Db 230 LGWSRSPRLQIPAMWTEDSGSYWCEVETVTHSIKRSLSRQIRVQ----- 274
QY 297 LNFEGTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVCRCGASISFSLTTENSQNYCT 356
Db 275 ----- 274
QY 357 ADNLGAKPSKAVSLSVTPVSHVPLNLSSPEDLIFEGAKVTLHCEAORGSLPILYQPHH 416
Db 275 -----RVFVSNVNLRIPTGGQLIEGNMVLICVAGSGSTVTFSSHK 317
QY 417 ED--AALERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSTVPSHPV 474
Db 318 EGRVRSLGRT-----QRSLLAEHL-----V 338
QY 475 LTLSSAELTFEGATVTLHCEVQSGPQLIYQFYHEDMPLMSSTPSVGRVSFSLTEG 534
Db 339 LTVKESDA----- 346
QY 535 HSGNYCTADNGFGPQSRSEWSLFTVTPVSRPILTLRPRAQAVVGDLLHCEAPRGSP 594
Db 347 --GRYYCAADNVHSPILSTWIRTVIPVSHVPLTFRAPRAHTVVGDLLHCESLRGSP 404
QY 595 PILYFYHEDVTLGSSAPSGGASPNLSLTAHSGNYSCEANGLVIAQHSOTISLSVTV 654
Db 405 PILYFYHEDVTLGNSAPSGGASPNLSLTAHSGNYSCEADNGLGASHGVSLRVTV 464
QY 655 PVSRLPILTRAPAAQAVGDLLHCEALRGSPILYFYHEDVTLGKISAPSGGASPN 714
Db 465 PVSRLPILTRAPAAQAVGDLLHCEALRGSPILYFYHEDVTLGKISAPSGGASPN 524
QY 715 LSLTTEHSGIYSCADNGLAORSEMVTLKAVPVSRLPILTRAPGTHAAVGDLLHCE 774
Db 525 LSLTT----- 529
QY 775 ALRGSPLILYRPFHEDVTLGNRSSPGGASLNLSTAEHSGNYSCEADNGLAORSETTV 834
Db 530 -----EHSNGNYSCEADNGLAORHKSQVTV 552
QY 835 LYITGLTANRSGPFATGAGLLSIAGLAAGALLLYCWLRSRAGKRP----- 881
Db 553 LNVGTSRNKTGLTAAGITGLVLSILVLAALH---YARARRPGGLSATGTSSHSP 609
QY 882 --ASDPARS-PSDSDSQEPTYNVPAWEELQPVYTANPRGENVYVSEVRIIQQEKKHAV 938
Db 610 SECEPSSSRPRIDQEPHPSKPLAPMELEPYSNVNPGDSNPYISQIWSIQTENSA 669
QY 939 ASDPRHLRNKGSPIIYSEVK 958
Db 670 NCPMMHQEHELTLYSELK 689

RESULT 15

ID AEM84916 standard; protein; 750 AA.
XX AC AEM84916;
XX DT 18-NOV-2004 (first entry)
XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:5165.
XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX OS Homo sapiens.
XX PN WO2004023973-A2.
XX PD 25-MAR-2004.

XX PF 12-SEP-2003; 2003WO-US028227.
XX PR 12-SEP-2002; 2002US-0410259P.
XX PA 12-SEP-2002; 2002US-0410260P.
XX (INCY-) INCYTE CORP.
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F, Harthshorne TA, Suchorolski MT, Altus CM, Pitte SJ, Elder LV, Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP, Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH, Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL, Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtson ES, Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D, Patry S, Shi X, Suarez CJ;
XX WPI; 2004-329368/30.
XX N-PSDB; ACN43568.
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.
XX Claim 27; Page; 190pp; English.
XX The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX Sequence 750 AA;
XX Query Match 30.1%; Score 1538.5; DB 8; Length 750;
XX Best Local Similarity 36.9%; Pred No. 9.2e-89;
XX Matches 362; Conservative 94; Mismatches 211; Indels 313; Gaps 14;
QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPWTTFQGRVTLTCGFRFPSPQ-KTKWYH 59
Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOPWTTFQGRVTLTCGFRFPSPQ-KTKWYH 60
QY 60 RYLKREILRETPDNLVEQESGEYECQAGSPVHLDFSSASILLQAPLSVPEGDSV 119
Db 61 ---DEKLKIKHDKT-QITEPGNYQCKRGSLSDAVHVEFSPDWLILQALHPVEGDV 116
QY 120 VLRCRAKAEVTLNNTYTKNDNVLAFLNKRDTDPHIFACIKDNGAYRCTGYKESC---CPV 176
Db 117 ILRCQCKDNKNTQKQVYKQGLQKLPNSYNLEKITVNSVSRDMSKYHCTAYRKFILDI 176
QY 177 SSNTVKIQVEPFTPRPVLRASSFPISGNPVTLCETQSLERSDVPLFRFRDQTLG 236
Db 177 TSKPLNIQVQELFLHPVLRASSTIEGSPMLTCTQSLSPQRPVQLOFSLFRDSTLIG 236
QY 237 LGWSLSPNFQITAMWSKDSGFYCKAAATPHSVISDSRSPWQIQVPIPAHPVLTLSPEKA 296
Db 237 LGWSRSPRLQIPAMWTEDSGSYWCEVETVTHSIKRSLSRQIRVQ----- 281
QY 297 LNFEGTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVCRCGASISFSLTTENSQNYCT 356
Db 282 ----- 281

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:27:40 ; Search time 32.7345 Seconds
(without alignments)
2227.987 Million cell updates/sec

Title: US-09-724-254A-41
Perfect score: 5116
Sequence: 1 MLLWVILLVLPVSGGFART.....KVASTPVSGSLFLASSAPHR 977

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3787.5	74.0	1248	4	US-09-949-016-10595
2	3787.5	74.0	1248	4	US-09-949-016-10596
3	412	8.1	4391	4	US-10-006-011A-2
4	386	7.5	261	4	US-09-245-764-7
5	359	7.0	1709	4	US-09-949-016-10503
6	351.5	6.9	738	3	US-08-478-208-32
7	351.5	6.9	738	4	US-09-336-536-73
8	344.5	6.7	738	6	5264554-2
9	344.5	6.7	738	6	5264554-2
10	316.5	6.2	698	2	US-08-602-725-36
11	316.5	6.2	702	4	US-09-949-016-6484
12	316.5	6.2	734	2	US-08-389-459A-17
13	316.5	6.2	734	3	US-08-987-867A-17
14	316.5	6.2	740	4	US-09-949-016-8168
15	305.5	6.0	254	2	US-08-667-939A-3
16	304.5	6.0	254	4	US-08-433-123-3
17	304.5	6.0	254	2	US-08-667-939A-2
18	304.5	6.0	254	4	US-08-433-123-2
19	294.5	5.8	642	1	US-08-217-299-1
20	293	5.7	233	2	US-08-667-939A-6
21	293	5.7	233	4	US-08-433-123-6
22	292.5	5.7	254	2	US-08-667-939A-9
23	292.5	5.7	254	4	US-08-433-123-9
24	292	5.7	233	2	US-08-667-939A-5
25	292	5.7	233	4	US-08-667-939A-8
26	292	5.7	233	4	US-08-433-123-5
27	292	5.7	233	4	US-08-433-123-8

28	290	5.7	315	4	US-09-949-016-11121	Sequence 11121, A
29	290	5.7	315	4	US-09-949-016-11122	Sequence 11122, A
30	288.5	5.6	254	2	US-08-667-939A-4	Sequence 4, Appli
31	288.5	5.6	254	4	US-08-433-123-4	Sequence 4, Appli
32	286	5.6	233	2	US-08-667-939A-7	Sequence 7, Appli
33	286	5.6	233	4	US-08-433-123-7	Sequence 7, Appli
34	285.5	5.6	254	2	US-08-667-939A-1	Sequence 1, Appli
35	285.5	5.6	254	4	US-08-433-123-1	Sequence 1, Appli
36	285	5.6	1395	3	US-09-540-245A-15	Sequence 15, Appli
37	284	5.6	1070	4	US-09-961-403-3	Sequence 3, Appli
38	283	5.5	917	1	US-08-245-295-2	Sequence 2, Appli
39	283	5.5	917	1	US-08-481-130-2	Sequence 2, Appli
40	283	5.5	917	1	US-08-656-384A-2	Sequence 2, Appli
41	283	5.5	917	1	US-08-485-604-2	Sequence 2, Appli
42	283	5.5	917	2	US-08-487-595-2	Sequence 2, Appli
43	275	5.4	197	3	US-08-788-954-2	Sequence 2, Appli
44	275	5.4	203	2	US-08-667-939A-20	Sequence 20, Appli
45	275	5.4	203	4	US-08-433-123-20	Sequence 20, Appli

ALIGNMENTS

RESULT 1

US-09-949-016-10595
; Sequence 10595, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10595
; LENGTH: 1248
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10595

Query Match 74.0%; Score 3787.5; DB 4; Length 1248;
Best Local Similarity 97.2%; Pred. No. 2.9e-317;
Matches 725; Conservative 0; Mismatches 0; Indels 21; Gaps 2;

QY	1	MLLWVILLVLPVSGGFARTPRIIIFLOPPWTVFQGERVTLTCKGRFYSPQTKWYHR	60
DB	476	MLLWVILLVLPVSGGFARTPRIIIFLOPPWTVFQGERVTLTCKGRFYSPQTKWYHR	535
QY	61	YLCKEILRETPDNILBQESGEYRCQAQSPVHLDFSSASLILQAPLSYFEGDSVV	120
DB	536	YLCKEILRETPDNILBQESGEYRCQAQSPVHLDFSSASLILQAPLSYFEGDSVV	595
QY	121	LRCRAKAEVTLNNYIKNDNVLAFLNKRITDFHIFHACLKNGAYRCTGYKESCCPVSSNT	180
DB	596	LRCRAKAEVTLNNYIKNDNVLAFLNKRITDFHIFHACLKNGAYRCTGYKESCCPVSSNT	655
QY	181	VKIQVQEPTRPVLRRASSFPQISGNPVTITCTQLSLERSDVLRRFFRDDDTGLGWS	240
DB	656	VKIQVQEPTRPVLRRASSFPQISGNPVTITCTQLSLERSDVLRRFFRDDDTGLGWS	715
QY	241	LSPNFOITAMWKSDFYWKCAATMPHSVITSDPSRWIOVQIPASHPVLTLSPKALNFE	300
DB	716	LSPNFOITAMWKSDFYWKCAATMPHSVITSDPSRWIOVQIPASHPVLTLSPKALNFE	775
QY	301	GTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVRCERGASISFSLTENSNGNYCTADNG	360

Db	776	GTQVTLHCETQSDSLRTLYRFYHGVPLRHKSVCRCGASISFSLTTENSGNYCTADNG	835
Qy	361	LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQPHHEDAA	420
Db	836	LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQPHHEDAA	895
Qy	421	LERRANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTVPVSHPVNLSSA	480
Db	896	LERRANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTVPVSHPVNLSSA	955
Qy	481	EALTFEGATVTLHCEVORGSPQILYQFVHEDMPLWSSSTPSVGRVSFSLTEGHSNGNY	540
Db	956	EALTFEGATVTLHCEVORGSPQILYQFVHEDMPLWSSSTPSVGRVSFSLTEGHSNGNY	1015
Qy	541	CTADNGFGPQRSSEVSVLFTVTVPSRPILTLRVPRAQAVVGDLELHCEAPRGSPPILYWF	600
Db	1016	CTADNGFGPQRSSEVSVLFTVTVPSRPILTLRVPRAQAVVGDLELHCEAPRGSPPILYWF	1073
Qy	601	YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI	660
Db	1074	YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI	1133
Qy	661	LTFRAPRAQAVVGDLELHCEALRGSSPILYFYHEDVTLGKISAPSGGASFNLSLTT	720
Db	1134	LTFRAPRAQAVVGDLELHCEALRGSSPILYFYHEDVTLGKISAPSGGASFNLSLTT	1174
Qy	721	HSGIYSCDADNGLEAQRSEMTLKA	746
Db	1175	HSGIYSCDADNGLEAQRSEMTLKA	1200
RESULT 2			
US-09-949-016-10596			
; Sequence 10596, Application US/09949016			
; Patent No. 6812339			
; GENERAL INFORMATION:			
; APPLICANT: VENTER, J. Craig et al.			
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED			
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF			
; FILE REFERENCE: CL001307			
; CURRENT APPLICATION NUMBER: US/09/949,016			
; CURRENT FILING DATE: 2000-04-14			
; PRIOR APPLICATION NUMBER: 60/241,755			
; PRIOR FILING DATE: 2000-10-20			
; PRIOR APPLICATION NUMBER: 60/237,768			
; PRIOR FILING DATE: 2000-10-03			
; PRIOR APPLICATION NUMBER: 60/231,498			
; PRIOR FILING DATE: 2000-09-08			
; NUMBER OF SEQ ID NOS: 207012			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 10596			
; LENGTH: 1248			
; TYPE: PRT			
; ORGANISM: Human			
US-09-949-016-10596			
Query Match			
Best Local Similarity 74.0%; Score 3787.5; DB 4; Length 1248;			
Matches 725; Conservative 0; Mismatches 0; Indels 21; Gaps 2;			
Qy	1	MLLWILLVLAPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPQKTKWYHR	60
Db	476	MLLWILLVLAPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPQKTKWYHR	535
Qy	61	YLKGEILRETPDNILEVOESGEYRCQAQGPLSPVHLDSSASLILOAPLSVPEGDSVV	120
Db	536	YLKGEILRETPDNILEVOESGEYRCQAQGPLSPVHLDSSASLILOAPLSVPEGDSVV	595
Qy	121	LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKONGAYRCTGYKESCCPVSSNT	180
Db	596	LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKONGAYRCTGYKESCCPVSSNT	655
Query Match			
Best Local Similarity 8.1%; Score 412; DB 4; Length 4391;			
Matches 221; Conservative 131; Mismatches 422; Indels 180; Gaps 44;			
Qy	23	PIIFLOPPWTVFQGERVTLCKGFRFYSPQK-TKWYHRYLKGKILRETPDNIL-----E	76
Db	2630	PIRIESSPTVEGQTLNLCVWAR--QFOAITWYKGGSLPSGRHQTHGSHLRHOMS	2687
Qy	77	VOESGEYRCQAQ-----GSP-----LSSPVHLDSSASLILOAPLSVF	114
Db	2688	VADSGEYVCRANNIDALEASIVSVPSAGSFPAGSGSMPIRIESSS-----HVA	2739
Qy	115	EGDSVVLRCRAKAEVTLNNTIYKNDNVLA--FLNKRTPDHPHACLKONGAYRC-----T	167

Db 2740 EGETLDLNCVVGQAHAQVTHKRGGLSPSHQTRGSRRLRLHHVSPADSGEYVCRVMGSS 2799
Qy 168 GYKESCCPV---SNTVKIOVQEPFTRPVLR--ASSFOPIGPNVPLTLC-----ETQLS 216
Db 2800 GPLEASVLVTEASGSNAHVPAFGGAPPIRIEISSSRVAEGQTLDLKCVPGQAHAQV 2859
Qy 217 LER--SDVPLRFRFRDDQTLGLGWSLSPNQITAMMSKSGFYWK-----AATMPSHV- 269
Db 2860 WHKRGGLPARHGVH-----GPLLRLNQVSPADSGEYSCQVTSSTGTLASVL 2907
Qy 270 ISDSPRWIOVQIPASHPVLTLSPEKALNFGTKVTLHCETOEDSLTLRYFHYEG--VP 327
Db 2908 VTIEPSPGPPIAPGLAQPIYIEASSHVTEGQTLDLNCVVGQA--HAQVTWYKRGGLSP 2966
Qy 328 LRHSVRCERGASISFSLTT--ENSGNYCTADNGLGAKPSKAVLSLTVPVSH----- 379
Db 2967 ARHOT---HGSQRLHLVSPADSGEYVCRASGPG--PEGEASFTVTPPSESSYRLR 3020
Qy 380 -PVNLSSPDLIPEGAQVTLHCEAQRGSLPILYQFHEDDAALERRSANSAGGVAISFSL 438
Db 3021 SPVISIDPPSSTVOQGQDAPFKCLIHDAAPISLEWKTRNQELEDNVHISPNGSIITVG 3080
Qy 439 T-AHSGNYYCTADNGCPQRSKAVLSITVPVSHPVLTLSAALTFEGATVTLHCEVQ 497
Db 3081 TRPSNHGTYRCVASNAYGVAQS--VYVLSVHGPP--VSVLPEGPVWVKVGAVTLEC-VS 3136
Qy 498 RGSQILYQFYHEDMPLWS--SSTPSVGRVSFSPSLTEGH-----SGNYCYTA 543
Db 3137 AGEPR-----SSARKTRISSTPA-KLEORTYGLMDSHVLQISSAKPSDAGTYVCLA 3187
Qy 544 DNGGPGORSEVSLFVTPVSRPILTLRVPRQAVV--GDLELHCEAPRGSPPILYW-- 599
Db 3188 QNALGTAQKQVEVIVDTGAMAPGAQVQAEAEALTVEAGHTATLRCSATGSPAPTIHWSK 3247
Qy 600 -----FYHEDVTLGSSASPGSEASFNLSITAEHSGNYSCEANGLVLAQHS-D-TISLSV 652
Db 3248 LRSPLPQHR-----LEGDTLIPRVAQDQSGQYICNATS--PAGHAETIILHV 3295
Qy 653 IVPVSRPILTFRAPRAQVVDLLEHCEALRGSSPILY-WFYHEDVTLGKISAPSGGA 711
Db 3296 ESP---PYATVPBHASVQAGETVQLOCLA-HGTPPLTFQW-----SRVSSSLPRA 3343
Qy 712 SPNLSL-----TTEHSGIYSCSEADNGLEAQRSEMVTLKVAVPVSRPVLTLRAPGTHA-- 763
Db 3344 TARNELLHFAAPEDSGRYRCRTNVKVGSAEAPQALLVQGPGLPATSIPAGSTPTVQ 3403
Qy 764 -----AVGDLELHC--BALRGSPILYRPFHEDVTLONRSSPSGGASLNLSTAHE 813
Db 3404 VTPQLETKSIGASVEFHCAVPSDQGTQL---RMFKGGQLPPGHSVQDGVLRIQNLQDSC 3460
Qy 814 SGNYSCEADNGLG-AQRS-ETVTLTYITGLTANRSGPFATGVAGLLSIAGLAAG 865
Db 3461 QGYTICQHGFGWKAQASQVIALPSVLINRTSVQTVVGVHAEFECLALG 3514

RESULT 4

US-09-245-764-7

; Sequence 7, Application US/09245764

; Patent No. 6675105

; GENERAL INFORMATION:

; APPLICANT: Hogarth, P. Mark

; APPLICANT: Powell, Maree S.

; APPLICANT: McKenzie, Ian P.C.

; APPLICANT: Maxwell, Kelly F.

; APPLICANT: Garrett, Thomas P.J.

; APPLICANT: Epa, Vidana

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF Fc RECEPTORS

; FILE REFERENCE: 4102-4

; CURRENT APPLICATION NUMBER: US/09/245,764

; CURRENT FILING DATE: 1999-02-05

; EARLIER APPLICATION NUMBER: 60/099,994

; EARLIER FILING DATE: 1998-09-11

; EARLIER APPLICATION NUMBER: 60/073,972

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 7

; LENGTH: 261

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-245-764-7

Query Match 7.5%; Score 386; DB 4; Length 261;

Best Local Similarity 35.7%; Pred. No. 5.9e-25;

Matches 95; Conservative 40; Mismatches 121; Indels 10; Gaps 6;

Qy 20 TPRPIIFLQPPWTVTFQGERVTLTKCGFRFVSPQKTKWYHRYLKKEILRETPD--NILE 76
Db 1 TTAVITLQPPWVSFQEEVTLHCEVHLHPGSSSTQWFVN--GTATQTSTPSTRTSAS 58
Qy 77 VQESGEYRCQAQSGPLSSPVHLDFSSASLILQAPLSVF-EGDSVYLCRAKAEVTLNNTI 135
Db 59 VNSGEYRCQGLSGRSDPIQLETHRGWLLQLQVSSRVFTEGEPLALRCHAWKDKLVYNVL 118
Qy 136 YKDNVLAFLNKRTDTHI PHACLKDNCAIRCTGKESCCPVSSNTVKIOVQEPFTRPVLR 195
Db 119 YYRNGKFKFFHWSNLTLTKTNISHNGTYHCSGMGKH--RYTSAGISVTVKELFPAPVLN 176
Qy 196 ASSFQF--ISGNPVTLTCTQLSLERSDPLRFRFRDDQTLGLCWSLSPNQITAMMSKD 254
Db 177 ASVTSPLEGNLVTLSCTETKLLKQRPGLQLYFSGYMGSKTL-RGRNTSSSEYQILTARRED 235
Qy 255 SGFYCKAAATMPHSVISDSRSPRIQV 280
Db 236 SGLYWCEAATEDGNVLKRSPELELQV 261

RESULT 5

US-09-949-016-10503

; Sequence 10503, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10503

; LENGTH: 1709

; TYPE: PRT

; ORGANISM: Human

; US-09-949-016-10503

Query Match 7.0%; Score 359; DB 4; Length 1709;

Best Local Similarity 23.0%; Pred. No. 2.5e-21;

Matches 231; Conservative 113; Mismatches 408; Indels 254; Gaps 50;

Qy 10 LAPVSGQFARTPRPIFL-----QPPWTVF-QGERVTLTKCGFRFYPQTKWYHRY 61
Db 413 LTPVLTAFLTAQGLGILHCSVVSEPLATLVLSHGHIILASTSGDSHSPR----PSGT 468
Qy 62 LGKEILR-ETPDNILEVQESGEYRCQAQSGPLSPVHLDF--SSASILQAPLSVFEQDS 118
Db 469 SGPNLSRLRLEIRD--LBETDSGEYKCSATNSLGNATSLDTPHANAARLLISPAAEWEGQA 526

Patent No. 6406884
 GENERAL INFORMATION:
 APPLICANT: Leiby, K.
 APPLICANT: McKay, C.
 APPLICANT: Bosone, S.
 TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
 FILE REFERENCE: 7853-144
 CURRENT APPLICATION NUMBER: US/09/336,536
 CURRENT FILING DATE: 1999-06-18
 NUMBER OF SEQ ID NOS: 75
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 73
 LENGTH: 738
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-336-536-73

Query Match 6.9%; Score 351.5; DB 4; Length 738;
 Best Local Similarity 22.6%; Pred. No. 2.9e-21;
 Matches 177; Conservative 120; Mismatches 336; Indels 151; Gaps 33;
 259 WCAATMPHSPVISDSRPSRWIQVQP-----WLGVLTLTLLCSLEGQENSFTINSVDMKSLDPTVQNGKNL 297
 Db 5 WAQATM-----WLGVLTLTLLCSLEGQENSFTINSVDMKSLDPTVQNGKNL 53
 298 N-----FEGTKVTLHCETQEDSLRTLYRPHYHGVPLRHKSVRCERGASISFSLTTE-----ASHPVLTLSPKAL 348
 Db 54 TLOCFADVSTTSHVKPOHML-----FYKDDVLFYNVSSMKSTESYFIPEIRIYDSGTYK 98
 349 -----NSGNYCTADNGLGAKPSKAVSLSTVPSHPVLNLSPPEDLIFEGAKVTLHCEAQ 404
 Db 99 VRIYDSGTCTVNNKKTATAYQLLVE-GVPSRVTLDKKEAI--QGGIVRVNCSVP 155
 405 RGLSLPILYOPH-----HEDAALERSANSAGGVAISFSLTAHSG--NYCTAD--NGFG 455
 Db 156 EERAPIHTTEKLENEKMKVKLRKNSRDQNFVLEFPVEQDRVLSFRQARIISGIIH 215
 456 PQRS-----KAVLSITVPVSHPVLTLSAEALTFEGATVTLHCEVQ-----RGSPOILYQF 507
 Db 216 MOTSESTKSELVTVTESFSTPKFHSPT-GMIMEGAQLHKICTIQTVLAQEPFELIIQ- 273
 508 YHEDMPLWSSSTPSVGRVSFSLTEGHSGNYCTADNFGPQSEVSLFVTVP--VSR 565
 Db 274 --KDKAIVAHNRHGNKAVSVMAWE-HSGNYTCKVSS--RISKVSSIVVNITELFSK 327
 566 PILTLRVRAQAVVGGDLLEHCEAPRSGPILYFWFHYHEDVTLGSSAPSGEASFNLSLT 625
 Db 328 PELESFTHLQD--GERLNLSCSIP-GAPPANFTIQKEDTIVSQTO-----DFTKIAS 377
 626 AEHSGNYSCANNGLVAQHSDDTISLSVIVPSRPILTFRAPRAQAVVGGDLLEHCEALRG 685
 Db 378 KSDSGTYICTAGIDKVKVKSNTQIVVCEMLSQPRISYDA-QPEVIKGTIEVRCESISG 436
 686 SSPILYWFHYHEDVTLKISAPSGGASFNLSLTHESGIYSCADN--GLEAQRSEMTVL 743
 Db 437 TLPISQLLKTSKLENSTKNSNDPAVFDKNDPTEDVE--YQCVADNCHSHAKMLSEVLRV 494
 744 KVAVPVSRPVLTLRAQVAAVGGDLLEHCEALRGSPILYRFFHYHEDVTLGNSSPSGGA 803
 Db 495 KVTAPVDEQVILSKV--VESGEDIVLQCAVNEGSGPIYKYRE-----KEGKPFYQM 548
 804 SLNLS-----LTAHSGNYSC-----EADNGLGAQRSETVTLITGLTANRSGPFATG 851
 Db 549 TSNATQAFWTKQKASKEQEYCTAFNRANHASSVPRSKILLTVRVI-LAPMKGLIAVV 607
 852 VAGGLSIAGLAGALLLYCWLRSKAGRK-----PASDPARSPDSQSEPTVYHNPVWEE 907
 Db 608 IIGVITALLIIAA-----KCYFLRKAKAKOMPVEMSRPAVPLNNSNKKMSDPNMEANSH 662
 908 -----LQPVVTNANPRGENVYSEVRILIQEKKKHAVASDPRHLRNKGSPIIYSE 956
 Db 663 YGHNDVRNHAMKPINDKPELNSDVQYTEVQV-----SSAESKDLGKKDTETVISE 715

957 VKVA 960
 Db 716 VRKA 719
 RESULT 8
 5264554-2
 Patent No. 5264554
 APPLICANT: Newman, Peter J.
 TITLE OF INVENTION: PLATELET CELL ADHESION MOLECULE AND
 VARIANTS THEREOF
 NUMBER OF SEQUENCES: 2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/466,140
 FILING DATE: 19-JAN-1990
 SEQ ID NO:2
 LENGTH: 738
 5264554-2

Query Match 6.7%; Score 344.5; DB 6; Length 738;
 Best Local Similarity 22.4%; Pred. No. 1.2e-20;
 Matches 173; Conservative 121; Mismatches 349; Indels 131; Gaps 31;
 259 WCAATMPHSPVISDSRPSRWIQVQP-----WLGVLTLTLLCSLEGQENSFTINSVDMKSLDPTVQNGKNL 297
 Db 5 WAQATM-----WLGVLTLTLLCSLEGQENSFTINSVDMKSLDPTVQNGKNL 53
 298 N-----FEGTKVTLHCETQEDSLRTLYRPHYHGVPLRHKSVRCERGASISFSLTTE-----ASHPVLTLSPKAL 348
 Db 54 TLOCFADVSTTSHVKPOHML-----FYKDDVLFYNVSSMKSTESYFIPEIRIYDSGTYK 108
 355 CTADNGLGAKPSKAVSLSTVPSHPVLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQF 414
 Db 109 CTIVANNKKTATAYQLLVE-GVPSRVTLDKKEAI--QGGIVRVNCSVPPEEKAPIHTI 165
 415 H-----HEDAALERSANSAGGVAISFSLTAHSG--NYCTAD--NGFGPQRS--KAV 462
 Db 166 EKLENEKMKVKLRKNSRDQNFVLEFPVEQDRVLSFRQARIISGIIHMTSESTKSE 225
 463 SLGITVPVSHPVLTLSAEALTFEGATVTLHCEVQ-----RGSPOILYQFVHEDMPLWSS 517
 Db 226 LVTVTESFSTPKFHSPT-GMIMEGAQLHKICTIQTVLAQEPFELIIQ--KDKAIVAH 281
 518 STPSVGRVSFSLTEGHSGNYCTADNFGPQSEVSLFVTVP--VSRPILTLRVRA 575
 Db 282 NRHGNKAVSVMAWE-HSGNYTCKVSS--RISKVSSIVVNITELFSKPELESSTH 337
 576 QAVVGGDLLEHCEAPRSGPILYFWFHYHEDVTLGSSAPSGEASFNLSLTAHSGNYSC 635
 Db 338 DG--GERLNLSCSIP-GAPPANFTIQKEDTIVSQTO-----DFTKIASKSDSGTYICT 387
 636 ANGLVAQHSDDTISLSVIVPSRPILTFRAPRAQAVVGGDLLEHCEALRGSPILYWFYH 695
 Db 388 AGIDKVKVKSNTQIVVCEMLSQPRISYDA-QPEVIKGTIEVRCESISGTLPIYSQLLK 446
 696 EDVTLGKISAPSGGASFNLSLTHESGIYSCADN--GLEAQRSEMTVLKVAVPVSRPV 753
 Db 447 TSKVLENSTKNSNDPAVFDKNDPTEDVE--YQCVADNCHSHAKMLSEVLRVKVIAPVDEVQ 504
 754 LTLRAQVAAVGGDLLEHCEALRGSPILYRFFHYHEDVTLGNRSPSGGASLNL 808
 Db 505 ISILSKV--VESGEQIVLQCAVNEGSGPIYKYRE-----KEGKPFYQMTSNATQAFWT 558
 809 ---LTAHSGNYSC-----EADNGLGAQRSETVTLITGLTANRSGPFATGAGGLSIA 861
 Db 559 KQASKEQEYCTAFNRANHASSVPRSKILLTVRVI-LAPMKGLIAVVIIIGVITALLI 617
 862 LAAGALLLYCWLRSKAGRK-----PASDPARSPDSQSEPTVYHNPVWEE----- 907
 Db 618 IAA-----KCYFLRKAKAKOMPVEMSRPAVPLNNSNKKMSDPNMEANSHYGHNDVRNH 672
 908 -LQPVVTNANPRGENVYSEVRILIQEKKKHAVASDPRHLRNKGSPIIYSEVKVA 960
 Db 908 -LQPVVTNANPRGENVYSEVRILIQEKKKHAVASDPRHLRNKGSPIIYSEVKVA 960

Db 673 AMKPINDNKEPLNSDVQYTEVQV-----SSAESHKDLGKDKTETVYSEVRKA 719

RESULT 9
5264554-2
; Patent No. 5264554
; APPLICANT: Newman, Peter J.
; TITLE OF INVENTION: PLATELET CELL ADHESION MOLECULE AND
; VARIANTS THEREOF
; NUMBER OF SEQUENCES: 2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/466,140
; FILING DATE: 19-JAN-1990
; SEQ ID NO:2
; LENGTH: 738
5264554-2
Query Match 6.7%; Score 344.5; DB 6; Length 738;
Best Local Similarity 22.4%; Pred. No. 1.2e-20;
Matches 173; Conservative 121; Mismatches 349; Indels 131; Gaps 31;
QY 259 WCKAATMPHSVSDSPRSVIOVQIP-----ASHPVLTLSPKAL 297
Db 5 WQAQATM-----WGLVLLTLCCSLLEGQENSFTINSVDMKSLPDMWTQVGNKL 53
QY 298 N----FEGTKVTLCHCTQEDSLRLYRFYHGVPLRHKSVCRCGASISFSLTTSNGYY 354
Db 54 TLQCFADVSTTSHVKPQHQL-----FYKDDLVFNYSMMKSTESYFIPFVRIYDSGT 108
QY 355 CTADNGLGAKPSKAVSLSTVPSVHPVNLSPEDLIFGAKVTLHCEAQRGLPLIYQF 414
Db 109 CTIVVNNKKTAEYQQLLVE-GVSPRVTLDKKEAI--OGGIVRVNCSVPEKAPIHFTI 165
QY 415 H----HEDAALERRSANSAGGVAISFSLTAHSG-----NYICTAD--NGFGPORS---KAV 462
Db 166 EKLELNKVKVLRKNSRDQNFVLEFPVEQDRVLSFRCAIISGIHMOTSESTKSE 225
QY 463 SLSITVPVSHPVVLTLSAALTFEGATVTLHCEVQ-----RGSPLLQYFYHEDMPLWS 517
Db 226 LVTVTESFSTPKFHISFT-GMIMEGALHKTCTIQTHTLAQEFPEIIQ---KDKAIVAH 281
QY 518 STFSVGRVSFSLTGHSGNYCTADNGFGPORSWSLFTVP--VSRPILTLRVPR 575
Db 282 NRHGNKAVYSWAMVZ-HSGNYTKVSS---RISKVSIVNITELFSKPELESFTHL 337
QY 576 QAVVGDLELHCEAPRGPPLIYFYHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCE 635
Db 338 DG--GERLNLSCSIP-GAPPANFTIQEDTIVSQIQ-----DFTKIASKSDSGTYICT 387
QY 636 ANGLVAQHSDDTSLSVIVPVSRLTFRAPRAQAVVGDLELHCEALRGSSPILYWFYH 695
Db 388 AGIDKVVYKSNTOIVVCEMLSPQISYDA-QEVIKGTIVKRCESISGTLPISTQLLK 446
QY 696 EDVTLGKISAPSGGASFNLSLTHSGIYSCEADN--GLEAQRSEMTLKVAVPVSFV 753
Db 447 TSKVLENTKNSNDPAVKFNPTEDVE--YQCVADNCHSHAKMLSEVLVKVIAVPDEVQ 504
QY 754 LTRAPGTHAAVGDLELHCEALRGSPPLIYFYHEDVTLGNSRSPSGGASINLS----- 808
Db 505 ISILSSKV-VESGQIVLQCAVNEQSGPITYKYRE-----KEGKPPYQMTSNATQAFWT 558
QY 809 ---LTAHSGNYS----EADNGLGAORSETVTLITGLTANSGPFPATGAGLLSIAG 861
Db 559 KQKASKQEQEYICTAFNRANHASSVPSKILITRVI-LAPWKGLIAVVIIGIALLI 617
QY 862 LAAGALLLYCWLRSKAGRK-----PASDPARSPSDSDQEPYTHNVPAWEE----- 907
Db 618 IAA-----KCYFLRKAKAKQMPVMSRPAPVLLNSNNEKMSDPNMEANSHYHNDVVRNH 672
QY 908 -LQPVYTNANPRGENVYSEVRIIOEKKHNAVADSPRLHAKGSPILYSEVKA 960
Db 673 AMKPINDNKEPLNSDVQYTEVQV-----SSAESHKDLGKDKTETVYSEVRKA 719

RESULT 10
US-08-602-725-36
; Sequence 36, Application US/08602725
; Patent No. 5965710
; GENERAL INFORMATION:
; APPLICANT: BODMER, WALTER F
; APPLICANT: DUBBIN, HELGA
; APPLICANT: SNARY, DAVID
; APPLICANT: STEWART, LORNA MD
; APPLICANT: YOUNG, SUSAN
; APPLICANT: BATES, PAUL A
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,725
; FILING DATE: 02-FEB-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB94/01816
; FILING DATE: 19-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9317423
; FILING DATE: 21-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36663
; REFERENCE/DOCKET NUMBER: 1090-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 698 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-602-725-36
Query Match 6.2%; Score 316.5; DB 2; Length 698;
Best Local Similarity 19.5%; Pred. No. 2.8e-18;
Matches 177; Conservative 119; Mismatches 331; Indels 283; Gaps 33;
QY 29 PFWTTFQGVERTLCKGFRFYSQKTKWYHRYLKEILRETPDNILEVQE----- 79
Db 3 PPHRCIPQWRLTLTASLLTFWNPPT-----AKLATIESTPFNVAEKVELLLVHNL 55
QY 80 -----SGY-----RCQAQGSPLSSPVHLDFFSSALILQAPLSVFEGD 117
Db 56 OHLFGYSWYKGRVDGNROIIGVGTQQTQATPGPAYSGREIYPNASLLIQ----- 106
QY 118 SVVLRCAKAEVTLNNTIYKNDNLVLAFLNKRDTDFHIFACLDKNGAYRCTGYKESCCPV 177
Db 107 -----NIIQND-----TGFVTLHVIKSDLVNEEATG----- 132
QY 178 SNTVKIQVQEPFTRPVLRASSQPTSG-NPVTLTCTQSLERSDVPLRFRFRDDOTLG 236
Db 133 ----QPRVYPELPKPSISSNNSKPKVEDKDAVFTCEP----- 166
QY 237 LGWSLSFNPQITAMWSKDSGFYCKAATMPHSVISDSPRSWIQVQIPASHPVLTLSPKA 296

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Db 167 -----TODATYLM-----WVNNQ-----SLPVSRLQ 188
Qy 297 LNFEGTKVTLHCETQEDSLRLRYFYHEGVPLRHKSVRCERGASISFSLTTENSNGNYCT 356
Db 189 LSNNGRTLTL-----FNVTRNDTASYKE 212
Qy 357 ADNLGLAKPSKAVSLSVTVVSHVPLNLSPEDLIF-EGAKVTLHCEAQRGSILYQFPH 415
Db 213 TONPVSARRSDSVILNLYGPDAPTI---SPLNTSYRSGENLNSCHA-ASNPPAQYSWF 268
Qy 416 ----HEDAALERRSANSAGGVAISFSLTAHSGNYCTADNG-FGPORSKAVSLSVTVV 470
Db 269 VNGTFQOSTQELFIPN-----ITVNSSGYTCQAHNSDTGLNRTTITVVAEP 318
Qy 471 SHPVLTLSSAEALTFEGATVTLHCEVORGSPQLYQFYHEDMPLW---SSSTPSVGRVSF 527
Db 319 PKPFIITNSNPVEDEDA-VALTCE-----PEIQNTTY-----LWVNNQSLPVSRLQ 367
Qy 528 S-----FSLTEHSGNYCTADNGFGPORSSEVSLFTV---PVSRPILTLRPRA 575
Db 368 SNDNRTLTLSSVTRNDVGPYECGIQNELSVDSHPVILNLYGPDPTISPSVTTYRP-- 425
Qy 576 QAVUGDLLELHCEAPRGSPILYFWFYHEDVTLGSSSAPSGEASFNLSLTAHSGNYSCE 635
Db 426 ----GVNLSLSCHAAASNPPAQYSWLDIGNIQHT-----QELFISNITEKNSGLYTCQ 474
Qy 636 ANGLVAQSDTISLSVIVPVSRLPILTFRAPRAQAVVG-DLLELHCEALRGSSPILYWFY 694
Db 475 ANNS-ASGHSRTTKITVSAELPKPSISSNNKPKVEDKDAVFTCEPEAQNTIYLWVN 533
Qy 695 HEDVTLGKISAPSGGASFNL-SLTTEHSGIYCEADNGLEAQRSEMVTILKAVPVSRLV 753
Db 534 GOSLPVSPRLQSLNGNRTLTLEFNTRNDARAYVCGIQNSVSNRSDPVLVDLYGPDPTI 593
Qy 754 LTRAPGTHAAVGDLELHCEALRGSPILYFRFHEVTLGNRSSPSGGASLNS----- 808
Db 594 IS--PPDSSYLSGANLNSCH-----SASNPSQYSWRINGIQQ 631
Qy 809 -----LTAEHSGNYSCEADNGLEAQRSETVTLITGLTANRSIVKSIIVSAGTSPGLSAGATVGM-- 688
Db 632 HTQVLFIAKITPNNGTYACFVSN-LATGRNNSIVKSIIVSAGTSPGLSAGATVGM-- 688
Qy 860 AGLAAGALL 869
Db 689 IGVLVGVALI 698
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RESULT 11

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US-09-949-016-6484
; Sequence 6484, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6484
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6484
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RESULT 12

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US-08-389-459A-17
; Sequence 17, Application US/08389459A
; Patent No. 5817512
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Query Match 6.2%; Score 316.5; DB 4; Length 702;
Best Local Similarity 19.5%; Pred. No. 2.8e-18;
Matches 177; Conservative 119; Mismatches 331; Indels 283; Gaps 33;
Qy 29 PWTTFQGERVTLTCKGFRFYSPQTKWHRVYLGKELRETDNILEVOE----- 79
Db 7 PPHRWCIPIQRLLUTLASLLTFMNPPTT-----AKLTIESTFNVAGKEVLLLVNLP 59
Qy 80 -----SGEY-----RCQAQGSPLSPVHLDFSSASLIILQAPLSVEGD 117
Db 60 QHLFGYSWYKGERVDGNRQIIGVIGTQATPGPAYSGREIILYPNASLLIQ----- 110
Qy 118 SVVLCRAKAEVTLNNTIYKDNVLAFLNKRTPHFPHACLKONGAYRCTGYKESCCPV 177
Db 111 -----NIQND-----TGFYTLHVIKSLDVNEEATG----- 136
Qy 178 SNTVKIQOVFPFPRVLRASSFOPISG-NPVTILTCETQLSLERSDVPRLRFRDDOTLG 236
Db 137 ----QRFVPELPKPSISSNNKPKVEDKDAVFTCEPE----- 170
Qy 237 LGWSLSPNFQITAMWKSQGFYWCKAATMPHSVISDSPRSWIOVQIPASHPVLTLSP 296
Db 171 -----TQDATYLM-----WVNNQ-----SLPVSRLQ 192
Qy 297 LNFEGTKVTLHCETQEDSLRLRYFYHEGVPLRHKSVRCERGASISFSLTTENSNGNYCT 356
Db 193 LSNNGRTLTL-----FNVTRNDTASYKE 216
Qy 357 ADNLGLAKPSKAVSLSVTVVSHVPLNLSPEDLIF-EGAKVTLHCEAQRGSILYQFPH 415
Db 217 TONPVSARRSDSVILNLYGPDAPTI---SPLNTSYRSGENLNSCHA-ASNPPAQYSWF 272
Qy 416 ----HEDAALERRSANSAGGVAISFSLTAHSGNYCTADNG-FGPORSKAVSLSVTVV 470
Db 273 VNGTFQOSTQELFIPN-----ITVNSSGYTCQAHNSDTGLNRTTITVVAEP 322
Qy 471 SHPVLTLSSAEALTFEGATVTLHCEVORGSPQLYQFYHEDMPLW---SSSTPSVGRVSF 527
Db 323 PKPFIITNSNPVEDEDA-VALTCE-----PEIQNTTY-----LWVNNQSLPVSRLQ 371
Qy 528 S-----FSLTEHSGNYCTADNGFGPORSSEVSLFTV---PVSRPILTLRPRA 575
Db 372 SNDNRTLTLSSVTRNDVGPYECGIQNELSVDSHPVILNLYGPDPTISPSVTTYRP-- 429
Qy 576 QAVUGDLLELHCEAPRGSPILYFWFYHEDVTLGSSSAPSGEASFNLSLTAHSGNYSCE 635
Db 430 ----GVNLSLSCHAAASNPPAQYSWLDIGNIQHT-----QELFISNITEKNSGLYTCQ 478
Qy 636 ANGLVAQSDTISLSVIVPVSRLPILTFRAPRAQAVVG-DLLELHCEALRGSSPILYWFY 694
Db 479 ANNS-ASGHSRTTKITVSAELPKPSISSNNKPKVEDKDAVFTCEPEAQNTIYLWVN 537
Qy 695 HEDVTLGKISAPSGGASFNL-SLTTEHSGIYCEADNGLEAQRSEMVTILKAVPVSRLV 753
Db 538 GOSLPVSPRLQSLNGNRTLTLEFNTRNDARAYVCGIQNSVSNRSDPVLVDLYGPDPTI 597
Qy 754 LTRAPGTHAAVGDLELHCEALRGSPILYFRFHEVTLGNRSSPSGGASLNS----- 808
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Qy 860 AGLAAGALL 869
Db 693 IGVLVGVALI 702
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us-09-724-254a-41.ra1

Thu May 5 15:11:00 2005

GENERAL INFORMATION:
 APPLICANT: Morrow, Casey D. and Porter, Donna, C.
 TITLE OF INVENTION: ENCAPSIDATED RECOMBINANT POLIOVIRUS
 TITLE OF INVENTION: NUCLEIC ACID AND METHODS OF MAKING AND
 TITLE OF INVENTION: USING SAME
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 STATE STREET, SUITE 510
 CITY: BOSTON
 STATE: MASSACHUSETTS
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/389,459A
 FILING DATE: 15-FEB-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/087,009
 FILING DATE: 01-JUL-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Silveri, Jean M.
 REGISTRATION NUMBER: 39,030
 REFERENCE/DOCKET NUMBER: UAG-004CP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 734 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-389-459A-17

Query Match 6.2%; Score 316.5; DB 2; Length 734;
 Best Local Similarity 19.5%; Pred. No. 3e-18;
 Matches 177; Conservative 119; Mismatches 331; Indels 283; Gaps 33;
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 39 PPHRCWCPQWRLTASLLTFWNPPTT-----AKLTISTPFWAEGKEVLLVHNLP 91
 80 -----SGEY-----RCQAQGSPLSPVHLDFFSSASLILOAPLSVPEGD 117
 92 QHLFGYSWYKGVGDGNQRIQYVIGTQATPGPAYSGREIIPNASLLIQ-----142
 118 SVVLCRAKAEVTLNNTIYKNDVLAFLNKTDPHIACKLKGAYRCTGYKESCCPVS 177
 143 -----NIQND-----TGFYTLHVKSILVNEAATG-----168
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 237 LGWSLSPNQITAMWKSQSGFYWCKAATMPHSVISDSPRSWIQVQIPASHVPLTLSPEKA 296
 203 -----TQDATYLM-----WVNNQ-----SLFVSPRLQ 224
 297 LNFEGTKVTLHCETOEDSLRTLYRFHGVPLRHKSVCERGASFSFLTTSNGNYCT 356
 225 LSGNRTLT-----FNVTRNDTASYKCE 248
 357 ADNLGAKESKAVLSVTVPVSHVPLNLSPPDLIF-EGAKVTLCEAQRGLSPILYQFH 415
 249 TQNPVSARRSDSVILNVLGPDAPTI---SPLNTSYRSGENLNLSCA-ASNPAPQYSWF 304

416 ---HEDAALEERSANSAGGVAISFSLTAHSGNYCYCTADNG-FGPORSKAVSUSITVPV 470
 305 VNGTQQSTQELFIEN-----ITVNSGSYTCQAHNSDTGLNRTTITVTVAEP 354
 471 SHPVLTLTSAEALTFEGATVTLHCEVQSGSQILYQFYHEDMPLM---SSSTPSVGRVSF 527
 355 PKPFTITSNNSNEVEDEDA-VALTCE-----PEIQNTTY-----LWVNNQSLPVSRLQL 403
 528 S-----FSLTEGHSNGNYCTADNGFGPQORSEVVSIFVTV---PVSRLTLTLRVPA 575
 404 SMDNRTLTLSSVTRNDVGVYEGCIQNELSVDSHPVILNVLVGPDDPTISPSYTYRP-- 461
 576 QAVVGDLELHCEAPRGSPPILYWFYHEDVTLGSSASPGGEASFNLSLTAHSGNYSCE 635
 462 ----GVNLSLSCHAAASNPAPQYSLIDGNIQHT-----QELFISNITEKNSGLYTCQ 510
 636 ANGLVAQHSDTISLSVIVPVSRLTTPAPRAQAVVG-DLLELHCEALRGSSPLIYMFY 694
 511 ANNS-ASGHSRTTKTITVSABLKPFSISSNNKPKVEDKDAVFTCEPEAQNTTYLWVN 569
 695 HEDVTGKISAPSGGASFNLSLTTESHSIYSCADNGLEAQRSEMVTLKVAVPVSRPV 753
 570 GQSLPVSRLQLSNGNRTLTLENVTENDARAYVCGIQNSVSNRSDPVTLDVLYGDDTPI 629
 754 LTLRAPGTHAAVGDLELHCEALRGSPILYRFFHEDVTLGNRSSPSGGASLNL 808
 630 IS--PPDSSYLSGANLNLSC-----SASNPSPQYSWRINGIPQ 667
 809 -----LTAHSGNYSCEADNGLGAORSETVTLITGLTANRSGPPATGVAGLLSI 859
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 860 AGLAAGALL 869
 725 IGVLVGVALI 734
 RESULT 13
 US-08-987-867A-17
 Sequence 17, Application US/08987867A
 Patent No. 6063384
 GENERAL INFORMATION:
 APPLICANT: C. Morrow et al.
 TITLE OF INVENTION: ENCAPSIDATED RECOMBINANT VIRAL
 TITLE OF INVENTION: NUCLEIC ACID AND METHODS OF MAKING AND
 TITLE OF INVENTION: USING SAME
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 28 STATE STREET
 CITY: BOSTON
 STATE: MASSACHUSETTS
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/987,867A
 FILING DATE: 09-DEC-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/087,009
 FILING DATE: 01-JUL-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Myers, Louis
 REGISTRATION NUMBER: 35,965
 REFERENCE/DOCKET NUMBER: UAP-004CPDV
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 742-4214

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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:38:21 ; Search time 103.659 Seconds
(without alignments)
3139.559 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	5116	100.0	977	15	US-10-057-475B-10462 Sequence 10462, A
3	5116	100.0	977	15	US-10-154-884B-10462 Sequence 10462, A
4	5116	100.0	977	15	US-10-403-847-9 Sequence 9, Appli
5	5116	100.0	977	16	US-10-764-324-10462 Sequence 10462, A
6	5104	99.8	977	14	US-10-241-220-97 Sequence 97, Appl
7	3923	76.7	759	14	US-10-040-862-10460 Sequence 10460, A
8	3923	76.7	759	15	US-10-057-475B-10460 Sequence 10460, A
9	3923	76.7	759	15	US-10-154-884B-10460 Sequence 10460, A
10	3923	76.7	759	15	US-10-403-847-7 Sequence 7, Appli
11	3923	76.7	759	16	US-10-764-324-10460 Sequence 10460, A
12	3897.5	76.2	790	15	US-10-403-847-4 Sequence 4, Appli
13	2962	57.9	592	14	US-10-040-862-10461 Sequence 10461, A

14	2962	57.9	592	15	US-10-057-475B-10461	Sequence 10461, A
15	2962	57.9	592	15	US-10-154-884B-10461	Sequence 10461, A
16	2962	57.9	592	15	US-10-403-847-8	Sequence 8, Appli
17	2962	57.9	592	16	US-10-764-324-10461	Sequence 10461, A
18	1854	36.2	438	15	US-10-403-847-6	Sequence 6, Appli
19	1559	30.5	707	15	US-10-108-260A-4774	Sequence 4774, Ap
20	1559	30.5	734	14	US-10-040-862-10463	Sequence 10463, A
21	1559	30.5	734	15	US-10-057-475B-10463	Sequence 10463, A
22	1559	30.5	734	15	US-10-154-884B-10463	Sequence 10463, A
23	1559	30.5	734	16	US-10-764-324-10463	Sequence 10463, A
24	1559	30.5	734	17	US-10-948-518-1137	Sequence 137, App
25	1541.5	30.1	727	17	US-10-473-519-20	Sequence 20, Appl
26	1502	29.4	317	15	US-10-403-847-2	Sequence 2, Appli
27	1411	27.6	592	15	US-10-162-335-94	Sequence 94, Appl
28	1205.5	23.6	639	16	US-10-408-765A-2410	Sequence 2410, Ap
29	931.5	18.2	508	14	US-10-040-862-10464	Sequence 10464, A
30	931.5	18.2	508	15	US-10-057-475B-10464	Sequence 10464, A
31	931.5	18.2	508	15	US-10-154-884B-10464	Sequence 10464, A
32	931.5	18.2	508	15	US-10-154-884B-11039	Sequence 11039, A
33	931.5	18.2	508	16	US-10-764-324-10464	Sequence 10464, A
34	931.5	18.2	508	17	US-10-948-518-1119	Sequence 119, App
35	900	17.6	181	16	US-10-363-829-286	Sequence 286, App
36	900	17.6	181	16	US-10-363-829-431	Sequence 431, App
37	884.5	17.3	327	15	US-10-363-616-458	Sequence 458, Appl
38	871.5	17.0	421	15	US-10-162-335-96	Sequence 96, Appl
39	871.5	17.0	421	15	US-10-162-335-98	Sequence 11043, A
40	864.5	16.9	445	15	US-10-154-884B-11043	Sequence 11043, A
41	861	16.8	460	15	US-10-154-884B-11048	Sequence 11048, A
42	851.5	16.6	421	15	US-10-162-335-100	Sequence 100, App
43	826.5	16.2	515	14	US-10-040-862-10459	Sequence 10459, A
44	826.5	16.2	515	15	US-10-057-475B-10459	Sequence 10459, A
45	826.5	16.2	515	15	US-10-154-884B-10459	Sequence 10459, A

ALIGNMENTS

RESULT 1

US-10-040-862-10462
; Sequence 10462, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416

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841 TANRSGPPATGVAGGLISIAAGALLIYCWLSKAGRPASDPARSPDSQSEPTIYH 900
901 NVPAMEELQPVYTNANPRGENVYSEVRIOEKKKHAVASDPRLHKNKGSPIIYSEKVA 960
901 NVPAMEELQPVYTNANPRGENVYSEVRIOEKKKHAVASDPRLHKNKGSPIIYSEKVA 960
961 STPVSGSLFLASSAPHR 977
961 STPVSGSLFLASSAPHR 977

RESULT 2

US-10-057-475B-10462
Sequence 10462, Application US/10057475B
Publication No. US20040002068A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Mannion, Jane
APPLICANT: Clapper, Jonathan David
APPLICANT: Wang, Aijun
APPLICANT: Ordonez, Nadia
APPLICANT: Carter, Lauren
APPLICANT: McNeill, Patricia Dianne
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-014402US
CURRENT APPLICATION NUMBER: US/10/057,475B
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 10979
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10462
LENGTH: 977
TYPE: PRT
ORGANISM: Homo sapiens
US-10-057-475B-10462

Query Match 100.0%; Score 5116; DB 15; Length 977;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MLLWVILLVLPVSGGFARTPRPIIFLOPPWTVTFQGERVTLTKGFRFYSPOKTKWYHR 60
1 MLLWVILLVLPVSGGFARTPRPIIFLOPPWTVTFQGERVTLTKGFRFYSPOKTKWYHR 60
61 YLKGKILRETPDNILEVQESGEYRCQAQSPVHLDFFSSASLILOAPLSVEGDSV 120
61 YLKGKILRETPDNILEVQESGEYRCQAQSPVHLDFFSSASLILOAPLSVEGDSV 120

PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10462
LENGTH: 977
TYPE: PRT
ORGANISM: Homo sapiens
US-10-040-862-10462
Query Match 100.0%; Score 5116; DB 14; Length 977;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MLLWVILLVLPVSGGFARTPRPIIFLOPPWTVTFQGERVTLTKGFRFYSPOKTKWYHR 60
1 MLLWVILLVLPVSGGFARTPRPIIFLOPPWTVTFQGERVTLTKGFRFYSPOKTKWYHR 60
61 YLKGKILRETPDNILEVQESGEYRCQAQSPVHLDFFSSASLILOAPLSVEGDSV 120
61 YLKGKILRETPDNILEVQESGEYRCQAQSPVHLDFFSSASLILOAPLSVEGDSV 120
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121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHAPHACLKNDGAYRCTGYKESCCPVSSNT 180
181 VKIQVQFPFRPVLRASSFOPIISGNPVTLTCETQLSLERSDVLPRFRFRDQTLGLGWS 240
181 VKIQVQFPFRPVLRASSFOPIISGNPVTLTCETQLSLERSDVLPRFRFRDQTLGLGWS 240
241 LSPNFOITAMWKSODSGFYWKCAATMPSHVSIDSRSWIOVQIPASHPVLTLSPKALNFE 300
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301 GTKVTLHCETQEDSLRTLYFYHEGVPLRHKSVCERCAGISFSLTENSNGNYCTADNG 360
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601 YHEDVTLGSSAPSGEASFNLSLTAHSGNYSCANNGLVAQHSDDTISLSVIVPSRPI 660
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781 LILYRPFHEDVTLGNSPSGGASLNLSTAHSGNYSCDANGLGCAQRSETVTLITGL 840

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Db 121 LRCRAEVTLNNTIYKNDNVLAFLNKRTDHPHACLKNDGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSFPISGNPVTLCETQLSLERSDVPLRFRFRDDQTLGLGWS 240
Db 181 VKIQVQEPFTRPVLRASSFPISGNPVTLCETQLSLERSDVPLRFRFRDDQTLGLGWS 240
QY 241 LSPNFOITAMWSKDSGFYCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
Db 241 LSPNFOITAMWSKDSGFYCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTLCETQEDSLRTLRYFHEGVPLRHKSVCERGASISFSLTTEGNYCTADNG 360
Db 301 GTKVTLCETQEDSLRTLRYFHEGVPLRHKSVCERGASISFSLTTEGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPLIYQPHHEDAA 420
Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPLIYQPHHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
QY 481 EALTFFEGATVTLHCEVQSGPOILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
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QY 541 CTADNGFGPQSEVSVLFTVTVPSRPILTILRVPAQAVVGDLLHCEAPRGSPPILYWF 600
Db 541 CTADNGFGPQSEVSVLFTVTVPSRPILTILRVPAQAVVGDLLHCEAPRGSPPILYWF 600
QY 601 YHEDVTLGSSAPSGGASFNLSLTAHSGNYSCAANGLVAQHSDTISLSVIVPSRPI 660
Db 601 YHEDVTLGSSAPSGGASFNLSLTAHSGNYSCAANGLVAQHSDTISLSVIVPSRPI 660
QY 661 LTRAPPAQAVVGDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT 720
Db 661 LTRAPPAQAVVGDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT 720
QY 721 HSGIYSCAENGLEAQRSEMTLKVAVPVSRLPVLTLRAPGTHAAVGLLHCEALRGSP 780
Db 721 HSGIYSCAENGLEAQRSEMTLKVAVPVSRLPVLTLRAPGTHAAVGLLHCEALRGSP 780
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Db 781 LILYRPFHEDVTLGNRSSPGGASLNLSTLAHSGNYSCAENGLEAQRSETVLYITGL 840
QY 841 TANRSGPFATGVAGLLSIAAGALLLYCWLRSRKAQRKPASDPARSDDSDSQEPTYH 900
Db 841 TANRSGPFATGVAGLLSIAAGALLLYCWLRSRKAQRKPASDPARSDDSDSQEPTYH 900
QY 901 NVPAWELQPVYTNANPRGENVYSEVRITIOEKKKHAVASDPRLRNKGSPIIYSEKVA 960
Db 901 NVPAWELQPVYTNANPRGENVYSEVRITIOEKKKHAVASDPRLRNKGSPIIYSEKVA 960
QY 961 STPVGSLFLASSAPHR 977
Db 961 STPVGSLFLASSAPHR 977
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RESULT 3
US-10-154-884B-10462
; Sequence 10462, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies

FILE REFERENCE: 014058-013521US
CURRENT APPLICATION NUMBER: US/10/154,884B
CURRENT FILING DATE: 2002-05-23
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-22
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-08-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 11290
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10462
LENGTH: 977
TYPE: PRT
ORGANISM: Homo sapiens
US-10-154-884B-10462

Query Match 100.0%; Score 5116; DB 15; Length 977;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 YLKEILRETPDNILEVQESGEYRCQAQSGPLSPVHLDPESSASLILQAPLSVPEGDSVV 120
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Db 181 VKIQVQEPFTRPVLRASSFPISGNPVTLCETQLSLERSDVPLRFRFRDDQTLGLGWS 240
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Db 241 LSPNFOITAMWSKDSGFYCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
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Db 301 GTKVTLCETQEDSLRTLRYFHEGVPLRHKSVCERGASISFSLTTEGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPLIYQPHHEDAA 420
Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPLIYQPHHEDAA 420
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Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
QY 481 EALTFFEGATVTLHCEVQSGPOILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
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Db 541 CTADNGFGPQSEVVSFLVTVPSRPILTLAVPRAQAVVGDLELHCEAPRGSPPILYWF 600
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Db 601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQSDTISLVIIPVSRPI 660
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QY LTFRAPRAQAVVGDLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720
Db 721 HSGIYSCEADNGLEAQRSEMTLVKAVPVSRLTLRAPGTHAAVGDLELHCEALRGSP 780
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QY LILYRFFHEDVTLGKISAPSGGASFNLSLTAHSGNYSCEADNGLEAQRSEMTLVKAVPVSRLTLRAPGTHAAVGDLELHCEALRGSP 900
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QY NVPAMEELQPVYTNANPRGENVYSEVRIIQEKKHAVASDPRLRNKGSPIIYSEVKVA 960
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QY STPVSGSLFLASSAPHR 977
Db 961 STPVSGSLFLASSAPHR 977

RESULT 4
US-10-403-847-9
; Sequence 9, Application US/10403847
; Publication No. US20040030098A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLICING VARIANTS OF A HUMAN
; TITLE OF INVENTION: CELL SURFACE PROTEIN WITH IMMUNOLOGICAL FOLDS, BGSSG AND BGSSG
; FILE REFERENCE: D0228 NP
; CURRENT APPLICATION NUMBER: US/10/403,847
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: U.S. 60/368,671
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: U.S. 60/371,420
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 9
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-847-9

Query Match 100.08; Score 5116; DB 15; Length 977;
Best Local Similarity 100.08; Pred. No. 0;
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLWVILLVLPVSGQFARTPRPIIFLOPPWTVTFQGERVLTCTCKGFRFYSPQTKWYHR 60
QY 61 YLGRKILRETPNILEVQESGYRQAGQSPVHLDFFSSALILQAPLVSVEGDSV 120
Db 61 YLGRKILRETPNILEVQESGYRQAGQSPVHLDFFSSALILQAPLVSVEGDSV 120
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Db 121 LECRAKAEVTLNNTIYKNDVLAFLNKRTHDHIHACILKNGAYRGTCTGKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSFPQISGNPVTCTCTQLSLERSDVPLRFRFRDDQTLGLWS 240

Db 181 VKIQVQEPFTRPVLRASSFPQISGNPVTCTCTQLSLERSDVPLRFRFRDDQTLGLWS 240
QY LSPNFOITAMWSDSGFYWCKAATWPHSVISDSRPSWQVQIPASHPVLTLSPEKALNFE 300
Db 241 LSPNFOITAMWSDSGFYWCKAATWPHSVISDSRPSWQVQIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTILHCEATQEDSLTLRYFVHEGVPLRHKSVRCERGASISFSLTENSNGNYCTADNG 360
Db 361 GTKVTILHCEATQEDSLTLRYFVHEGVPLRHKSVRCERGASISFSLTENSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTVPSVHPVNLNLSPELIIPEGAKVTLHCEAQRGLPILYQFHEDAA 420
Db 421 LGAKPSKAVSLSVTVPSVHPVNLNLSPELIIPEGAKVTLHCEAQRGLPILYQFHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYSCTADNGFGPQSKAVSLTITVPSHPVLTLSA 480
Db 481 LERRSANSAGGVAISFSLTAHSGNYSCTADNGFGPQSKAVSLTITVPSHPVLTLSA 480
QY 481 EALTFFEGATVTLHCEVQSGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
Db 541 EALTFFEGATVTLHCEVQSGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
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Db 721 HSGIYSCEADNGLEAQRSEMTLVKAVPVSRLTLRAPGTHAAVGDLELHCEALRGSP 780
QY 781 LILYRFFHEDVTLGKISAPSGGASFNLSLTAHSGNYSCEADNGLEAQRSEMTLVKAVPVSRLTLRAPGTHAAVGDLELHCEALRGSP 840
Db 781 LILYRFFHEDVTLGKISAPSGGASFNLSLTAHSGNYSCEADNGLEAQRSEMTLVKAVPVSRLTLRAPGTHAAVGDLELHCEALRGSP 840
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Db 841 TANRSGPFATGVAGGLSLTAGLAAGALLLYCWLRSKAGRKPAASDPARSPSDSQEPYTH 900
QY 901 NVPAMEELQPVYTNANPRGENVYSEVRIIQEKKHAVASDPRLRNKGSPIIYSEVKVA 960
Db 901 NVPAMEELQPVYTNANPRGENVYSEVRIIQEKKHAVASDPRLRNKGSPIIYSEVKVA 960
QY 961 STPVSGSLFLASSAPHR 977
Db 961 STPVSGSLFLASSAPHR 977

RESULT 5
US-10-764-324-10462
; Sequence 10462, Application US/10764324
; Publication No. US20040175739A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/764,324
; PRIOR FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126

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; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10462
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-324-10462

Query Match      100.0%; Score 5116; DB 16; Length 977;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPOKTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPOKTKWYHR 60
QY 61 YLGEKILRETPDNILEVQESGECYRCAQGSPLSPVHLDFFSSASLILQAPLSVFEQDSVV 120
DB 61 YLGEKILRETPDNILEVQESGECYRCAQGSPLSPVHLDFFSSASLILQAPLSVFEQDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDFHIFHACLDKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDFHIFHACLDKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVEPFRPVLRASSFOPIISGNPNVTLTCTQLSLERSDVLPRFRFRDDOTLGLWS 240
DB 181 VKIQVEPFRPVLRASSFOPIISGNPNVTLTCTQLSLERSDVLPRFRFRDDOTLGLWS 240
QY 241 LSPNFQITAMWSKDSGYWCKAATMPSHVSIDSPSRWIQVOIPASHPVLTLSEKALNFE 300
DB 241 LSPNFQITAMWSKDSGYWCKAATMPSHVSIDSPSRWIQVOIPASHPVLTLSEKALNFE 300
QY 301 GTRVTLHCETQEDSLRTLYRFYHEGVPLRHKSVCRCGASISFSLTENSNGNYCTADNG 360
DB 301 GTRVTLHCETQEDSLRTLYRFYHEGVPLRHKSVCRCGASISFSLTENSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHVPLNLSGPDILFEGAKVTLHCEAQRGSLPLIYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTPVSHVPLNLSGPDILFEGAKVTLHCEAQRGSLPLIYQFHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTPVSHVPLTLSSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTPVSHVPLTLSSA 480
QY 481 EALTFFEGATVTLHCEVORGSPQILYFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
DB 481 EALTFFEGATVTLHCEVORGSPQILYFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
QY 541 CTADNGFGPQRSVSLFVTVPSRPIITLRLVPRPRAQAVVGDLLLEHCEAPRGSPPIIYWF 600
DB 541 CTADNGFGPQRSVSLFVTVPSRPIITLRLVPRPRAQAVVGDLLLEHCEAPRGSPPIIYWF 600
QY 601 YHEDVTLGSSASPGGEASFNLSLTAHSGNYSCEANGLVAOHSOTISLSVIVPSRPI 660
DB 601 YHEDVTLGSSASPGGEASFNLSLTAHSGNYSCEANGLVAOHSOTISLSVIVPSRPI 660

661 LTFRAPRAQAVVGDLLLEHCEALRGSPPIIYWFYHEDVTLGKISAPSGGASFNLSLTTTE 720
661 LTFRAPRAQAVVGDLLLEHCEALRGSPPIIYWFYHEDVTLGKISAPSGGASFNLSLTTTE 720
721 HSGIYSCDADNGLEAQRSEWVTLKVAVPVSRPVLTLRAPGTHAAVGDLLLEHCEALRGSP 780
721 HSGIYSCDADNGLEAQRSEWVTLKVAVPVSRPVLTLRAPGTHAAVGDLLLEHCEALRGSP 780
781 LILYRPFHEDVTLGNRSSPSGGASLNLSTAEHSGNYSCEADNGLGARSETVTLYITGL 840
781 LILYRPFHEDVTLGNRSSPSGGASLNLSTAEHSGNYSCEADNGLGARSETVTLYITGL 840
841 TANRSGPFATGVAGLLSIAGLALLLWLSRKAGRKPAADPARSPSDSDSQEPTYH 900
841 TANRSGPFATGVAGLLSIAGLALLLWLSRKAGRKPAADPARSPSDSDSQEPTYH 900
901 NVPAMELQPVYTNANPRGENVYSEVRITIQEKKHAAVADPRHLRNKGGSPPIIYSEVKVA 960
901 NVPAMELQPVYTNANPRGENVYSEVRITIQEKKHAAVADPRHLRNKGGSPPIIYSEVKVA 960
961 STPVSGSLFLASSAPHR 977
961 STPVSGSLFLASSAPHR 977

RESULT 6
US-10-241-220-97
; Sequence 97, Application US/10241220
; Publication No. US20030148408A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: F5010R1-US
; CURRENT APPLICATION NUMBER: US/10/241,220
; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 97
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-241-220-97

Query Match      99.8%; Score 5104; DB 14; Length 977;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 975; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPOKTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPOKTKWYHR 60
QY 61 YLGEKILRETPDNILEVQESGECYRCAQGSPLSPVHLDFFSSASLILQAPLSVFEQDSVV 120
DB 61 YLGEKILRETPDNILEVQESGECYRCAQGSPLSPVHLDFFSSASLILQAPLSVFEQDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDFHIFHACLDKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDFHIFHACLDKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVEPFRPVLRASSFOPIISGNPNVTLTCTQLSLERSDVLPRFRFRDDOTLGLWS 240
DB 181 VKIQVEPFRPVLRASSFOPIISGNPNVTLTCTQLSLERSDVLPRFRFRDDOTLGLWS 240
QY 241 LSPNFQITAMWSKDSGYWCKAATMPSHVSIDSPSRWIQVOIPASHPVLTLSEKALNFE 300
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Thu May 5 15:11:00 2005

us-09-724-254a-41.rapb

241 LSPNFQITAMWSKDSGFYWCACKAATMPHSVSDSPRSMTQVQIPASHPVLTLSPEKALNFE 300
301 GTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVCRCGASISFSLTTSNGNYCTADNG 360
301 GTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVCRCGASISFSLTTSNGNYCTADNG 360
361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420
361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420
421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFQQRKAVSLSVTPVSHPVLTLSA 480
421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFQQRKAVSLSVTPVSHPVLTLSA 480
481 EALTPEGATVTLHCEVQRGSPQILYQFHYHEDMPLSSSTPSVGRVSFSLTEGHSNGY 540
481 EALTPEGATVTLHCEVQRGSPQILYQFHYHEDMPLSSSTPSVGRVSFSLTEGHSNGY 540
541 CTADNGFGQRSEVSLFVTPVSRPILTLRVPRAQAVVGDLLLEHCEAPRGSPPILYWF 600
541 CTADNGFGQRSEVSLFVTPVSRPILTLRVPRAQAVVGDLLLEHCEAPRGSPPILYWF 600
601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI 660
601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI 660
661 LTPRAQAVVGDLLLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLSTE 720
661 LTPRAQAVVGDLLLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLSTE 720
721 HSGIYSCADNGLEAQRSEMTVLKAVPVSRPILTLRAGTHAAVGDLLLEHCEALRGSP 780
721 HSGIYSCADNGLEAQRSEMTVLKAVPVSRPILTLRAGTHAAVGDLLLEHCEALRGSP 780
781 LILYRPFHEDVTLGNRSSPSGGASLNLSTAHSNYSCEADNGLCAQSRSETVLYITGL 840
781 LILYRPFHEDVTLGNRSSPSGGASLNLSTAHSNYSCEADNGLCAQSRSETVLYITGL 840
841 TANRSGPFATGVAGGLSLIAGLALLYCWLSRKAGRKAPSDPARSDSDSQBPTH 900
841 TANRSGPFATGVAGGLSLIAGLALLYCWLSRKAGRKAPSDPARSDSDSQBPTH 900
901 NVPABEQLQPVYTNANRGENVYSEVRILIQEKKHAAVADSDPHLKNKGSPIIYSEKVA 960
901 NVPABEQLQPVYTNANRGENVYSEVRILIQEKKHAAVADSDPHLKNKGSPIIYSEKVA 960
961 STPVSGSLFLASSAPHR 977
961 STPVSGSLFLASSAPHR 977

RESULT 7
US-10-040-862-10460
; Sequence 10460, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE OF INVENTION: Hematological Malignancies.
; FILE REFERENCE: 014058-0135200S
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303

PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10460
LENGTH: 759
TYPE: PRT
ORGANISM: Homo sapiens
US-10-040-862-10460

Query Match 76.7%; Score 3923; DB 14; Length 759;
Best Local Similarity 100.0%; Pred. No. 7.6e-266;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLQPPWTVFQGERVTLTKGPRFSPQTKWYHR 60
DB 1 MLLWVILLVAPVSGQFARTPRPIIFLQPPWTVFQGERVTLTKGPRFSPQTKWYHR 60
QY 61 YLGEIILRETDPNLTLEVOESGEYRCQAGSPVHLDFSSALIIQAPLSVFEQGSV 120
DB 61 YLGEIILRETDPNLTLEVOESGEYRCQAGSPVHLDFSSALIIQAPLSVFEQGSV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLKONGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLKONGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSQFIPISGNPVTLCETOLSLERSDPLRFRFRDDQTLGLGWS 240
DB 181 VKIQVQEPFTRPVLRASSQFIPISGNPVTLCETOLSLERSDPLRFRFRDDQTLGLGWS 240
QY 241 LSPNFQITAMWSKDSGFYWCACKAATMPHSVSDSPRSMTQVQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYWCACKAATMPHSVSDSPRSMTQVQIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVCRCGASISFSLTTSNGNYCTADNG 360
DB 301 GTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVCRCGASISFSLTTSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFQQRKAVSLSVTPVSHPVLTLSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFQQRKAVSLSVTPVSHPVLTLSA 480
QY 481 EALTPEGATVTLHCEVQRGSPQILYQFHYHEDMPLSSSTPSVGRVSFSLTEGHSNGY 540
DB 481 EALTPEGATVTLHCEVQRGSPQILYQFHYHEDMPLSSSTPSVGRVSFSLTEGHSNGY 540
QY 541 CTADNGFGQRSEVSLFVTPVSRPILTLRVPRAQAVVGDLLLEHCEAPRGSPPILYWF 600
DB 541 CTADNGFGQRSEVSLFVTPVSRPILTLRVPRAQAVVGDLLLEHCEAPRGSPPILYWF 600
QY 601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI 660
DB 601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI 660

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Db 601 YHEDVTLGSSAPSGGASFNLSLTAHSGNYSCEANNGLVLAHQSDTISLSVIVPSRPI 660
Qy 661 LTFRAPRAQAVVGDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTTE 720
Db 661 LTFRAPRAQAVVGDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTTE 720
Qy 721 HSGIYSCAADNGLEAQRSEMWTLKVA 746
Db 721 HSGIYSCAADNGLEAQRSEMWTLKVA 746

RESULT 8
US-10-057-475B-10460
; Sequence 10460, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-10460

Query Match 76.7%; Score 3923; DB 15; Length 759;
Best Local Similarity 100.0%; Pred. No. 7.6e-266;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLWILLVLAPVSGGOFARTPRIIFLOPPWTTVFQGERVTLTKCKGRFYSPOKTKWYHR 60
Db 1 MLLWILLVLAPVSGGOFARTPRIIFLOPPWTTVFQGERVTLTKCKGRFYSPOKTKWYHR 60
Qy 61 YLGEKILRETFDNIYQVESGEYRCQAQGSPLSPVHLDPFSSASLILQAPLSVFEGDSVV 120
Db 61 YLGEKILRETFDNIYQVESGEYRCQAQGSPLSPVHLDPFSSASLILQAPLSVFEGDSVV 120
Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRQTDPHIACLDKNGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRQTDPHIACLDKNGAYRCTGYKESCCPVSSNT 180
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Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRQTDPHIACLDKNGAYRCTGYKESCCPVSSNT 180
Qy 181 VKIQVQEPFTRPVLRASSFOPIISGNPVTLTCTETQLSLERSDVLPRFRFFRDOOTLGLGWS 240
Db 181 VKIQVQEPFTRPVLRASSFOPIISGNPVTLTCTETQLSLERSDVLPRFRFFRDOOTLGLGWS 240
Qy 241 LSPNFOITAMWSKDSGFYWCKAATMPHSVSDSPRSWIQVOIPASHPVLTLSPKALNPE 300
Db 241 LSPNFOITAMWSKDSGFYWCKAATMPHSVSDSPRSWIQVOIPASHPVLTLSPKALNPE 300
Qy 301 GTKVTILHCEQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTSTENGNYCTADNG 360
Db 301 GTKVTILHCEQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTSTENGNYCTADNG 360
Qy 361 LGAKPSKAVSLSVTVVPSHPVLNLSPPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Db 361 LGAKPSKAVSLSVTVVPSHPVLNLSPPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Qy 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVVPSHPVLTLSSA 480
Db 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVVPSHPVLTLSSA 480
Qy 481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLSLTGHSNYY 540
Db 481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLSLTGHSNYY 540
Qy 541 CTADNGFGPQRSVWSLFTVPSRPIILTLRVPAQAVVGDLLHCEAQRGSPPIIYWF 600
Db 541 CTADNGFGPQRSVWSLFTVPSRPIILTLRVPAQAVVGDLLHCEAQRGSPPIIYWF 600
Qy 601 YHEDVTLGSSAPSGGASFNLSLTAHSGNYSCEANNGLVLAHQSDTISLSVIVPSRPI 660
Db 601 YHEDVTLGSSAPSGGASFNLSLTAHSGNYSCEANNGLVLAHQSDTISLSVIVPSRPI 660
Qy 661 LTFRAPRAQAVVGDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTTE 720
Db 661 LTFRAPRAQAVVGDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTTE 720
Qy 721 HSGIYSCAADNGLEAQRSEMWTLKVA 746
Db 721 HSGIYSCAADNGLEAQRSEMWTLKVA 746

RESULT 9
US-10-154-884B-10460
; Sequence 10460, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
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us-09-724-254a-41.rapb

Thu May 5 15:11:00 2005

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; Sequence 7, Application US/10403847
; Publication NO. US20040030098A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLICED VARIANTS OF A HUMAN
; TITLE OF INVENTION: CELL SURFACE PROTEIN WITH IMMUNOLOGICAL FOLDS, BGS5G AND BGS51
; FILE REFERENCE: D0228 NP
; CURRENT APPLICATION NUMBER: US/10/403,847
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: U.S. 60/368,671
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: U.S. 60/371,420
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-403-847-7

Query Match          76.7%; Score 3923; DB 15; Length 759;
Best Local Similarity 100.0%; Pred. No. 7,6e-266;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWVILLVLPVSGGFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSQKTKWYHR 60
DB 1 MLLWVILLVLPVSGGFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSQKTKWYHR 60
QY 61 YLGEKILRETPDNILVQESGEYRCQAQSPVHLDPFSSASLILQAPLSVFEQDSVV 120
DB 61 YLGEKILRETPDNILVQESGEYRCQAQSPVHLDPFSSASLILQAPLSVFEQDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSFPISGNPVTLTCTQSLERSDPLRFRFRDDDTGLGWS 240
DB 181 VKIQVQEPFTRPVLRASSFPISGNPVTLTCTQSLERSDPLRFRFRDDDTGLGWS 240
QY 241 LSPNFQITAMWSKDSGFYCKAATPHSVISDSRPMIQQVQIPASHPVLTLSPKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYCKAATPHSVISDSRPMIQQVQIPASHPVLTLSPKALNFE 300
QY 301 GTKVTLCETQEDSLRTLRYFHEGVPLRHKSVCERGASISFSLTENSNGNYCTADNG 360
DB 301 GTKVTLCETQEDSLRTLRYFHEGVPLRHKSVCERGASISFSLTENSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGLPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGLPILYQFHEDAA 420
QY 421 LERRANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
DB 421 LERRANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
QY 481 EALTPEGATVTLHCEVQSGPQILYQFHEDMPLWSSSTPSVGRVSFSLTEGHSNGY 540
DB 481 EALTPEGATVTLHCEVQSGPQILYQFHEDMPLWSSSTPSVGRVSFSLTEGHSNGY 540
QY 541 CTADNGFGPQRSSEVSVLFTVPVSRPILTLVPRQAQVVGDLLEHCEAPRGSPPILYWF 600
DB 541 CTADNGFGPQRSSEVSVLFTVPVSRPILTLVPRQAQVVGDLLEHCEAPRGSPPILYWF 600
QY 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLVIIVPSRPI 660
DB 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLVIIVPSRPI 660
QY 661 LTFRAPRAQAVVGDLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720
DB 661 LTFRAPRAQAVVGDLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720

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; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-154-884B-10460

Query Match          76.7%; Score 3923; DB 15; Length 759;
Best Local Similarity 100.0%; Pred. No. 7,6e-266;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWVILLVLPVSGGFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSQKTKWYHR 60
DB 1 MLLWVILLVLPVSGGFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSQKTKWYHR 60
QY 61 YLGEKILRETPDNILVQESGEYRCQAQSPVHLDPFSSASLILQAPLSVFEQDSVV 120
DB 61 YLGEKILRETPDNILVQESGEYRCQAQSPVHLDPFSSASLILQAPLSVFEQDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSFPISGNPVTLTCTQSLERSDPLRFRFRDDDTGLGWS 240
DB 181 VKIQVQEPFTRPVLRASSFPISGNPVTLTCTQSLERSDPLRFRFRDDDTGLGWS 240
QY 241 LSPNFQITAMWSKDSGFYCKAATPHSVISDSRPMIQQVQIPASHPVLTLSPKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYCKAATPHSVISDSRPMIQQVQIPASHPVLTLSPKALNFE 300
QY 301 GTKVTLCETQEDSLRTLRYFHEGVPLRHKSVCERGASISFSLTENSNGNYCTADNG 360
DB 301 GTKVTLCETQEDSLRTLRYFHEGVPLRHKSVCERGASISFSLTENSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGLPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGLPILYQFHEDAA 420
QY 421 LERRANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
DB 421 LERRANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
QY 481 EALTPEGATVTLHCEVQSGPQILYQFHEDMPLWSSSTPSVGRVSFSLTEGHSNGY 540
DB 481 EALTPEGATVTLHCEVQSGPQILYQFHEDMPLWSSSTPSVGRVSFSLTEGHSNGY 540
QY 541 CTADNGFGPQRSSEVSVLFTVPVSRPILTLVPRQAQVVGDLLEHCEAPRGSPPILYWF 600
DB 541 CTADNGFGPQRSSEVSVLFTVPVSRPILTLVPRQAQVVGDLLEHCEAPRGSPPILYWF 600
QY 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLVIIVPSRPI 660
DB 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLVIIVPSRPI 660
QY 661 LTFRAPRAQAVVGDLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720
DB 661 LTFRAPRAQAVVGDLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720
QY 721 HSGIYSCDADNGLEAQRSEMTLKV 746
DB 721 HSGIYSCDADNGLEAQRSEMTLKV 746

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Qy 721 HSGIYSCADNGLEAQRSEMTLKVA 746
Db 721 HSGIYSCADNGLEAQRSEMTLKVA 746

RESULT 11
US-10-764-324-10460
; Sequence 10460, Application US/10764324
; Publication No. US20040175739A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/764,324
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-324-10460

Query Match 76.7%; Score 3923; DB 16; Length 759;
Best Local Similarity 100.0%; Pred. No. 7.6e-266;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPOKTKWYHR 60
Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPOKTKWYHR 60

Qy 61 YLCKEILRETPDNILEVQESGEYRCQAQSGPLSSPVHLDFFSSASLILQAPLSVFGDSVV 120
Db 61 YLCKEILRETPDNILEVQESGEYRCQAQSGPLSSPVHLDFFSSASLILQAPLSVFGDSVV 120

Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFHACLKNGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFHACLKNGAYRCTGYKESCCPVSSNT 180

Qy 181 VKIQVEPFRPVLRASSFPISGNPVTLTCTETQLSLERSDVLFRFRDDOTGLGWS 240
Db 181 VKIQVEPFRPVLRASSFPISGNPVTLTCTETQLSLERSDVLFRFRDDOTGLGWS 240

Qy 241 LSNFQITAMWSKDSGYWCKAATMPHSVLSDSPRSNIQVQIPASHPVLTLSPKALNPE 300
Db 241 LSNFQITAMWSKDSGYWCKAATMPHSVLSDSPRSNIQVQIPASHPVLTLSPKALNPE 300

Qy 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCRCERGASISFSLTTTENGSGNYCTADNG 360
Db 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCRCERGASISFSLTTTENGSGNYCTADNG 360

Qy 361 LGAKPSKAVSLSVTPVSHHPVLNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHHDDAA 420
Db 361 LGAKPSKAVSLSVTPVSHHPVLNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHHDDAA 420

Qy 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSA 480
Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSA 480

Qy 481 EALTFFEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
Db 481 EALTFFEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540

Qy 541 CTADNGFGPQSRSEVSLFVTVPSRPLTLRVPRQAQVGDLLLELHCEAPRGSPILYWF 600
Db 541 CTADNGFGPQSRSEVSLFVTVPSRPLTLRVPRQAQVGDLLLELHCEAPRGSPILYWF 600

Qy 601 YHEDVTLGSSSAPSGGEASFNLSTAEHSGNYSCAANNGLVAQHSDTISLSVIVPVSRIPI 660
Db 601 YHEDVTLGSSSAPSGGEASFNLSTAEHSGNYSCAANNGLVAQHSDTISLSVIVPVSRIPI 660

Qy 661 LTPRAPRAQAVVGDLLLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTTE 720
Db 661 LTPRAPRAQAVVGDLLLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTTE 720

Qy 721 HSGIYSCADNGLEAQRSEMTLKVA 746
Db 721 HSGIYSCADNGLEAQRSEMTLKVA 746

RESULT 12
US-10-403-847-4
; Sequence 4, Application US/10403847
; Publication No. US20040030098A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLICER VARIANTS OF A HUMAN
; TITLE OF INVENTION: CELL SURFACE PROTEIN WITH IMMUNOLOGOBULIN FOLDS, BGS5G AND BGS5I
; FILE REFERENCE: D0228 NP
; CURRENT APPLICATION NUMBER: US/10/403,847
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: U.S. 60/368,671
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: U.S. 60/371,420
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 790
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-847-4

Query Match 76.2%; Score 3897.5; DB 15; Length 790;
Best Local Similarity 96.0%; Pred. No. 4.9e-264;
Matches 746; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

Qy 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPOKTKWYHR 60
Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPOKTKWYHR 60

Qy 61 YLCKEILRETPDNILEVQESGEYRCQAQSGPLSSPVHLDFFSSASLILQAPLSVFGDSVV 102
Db 61 YLCKEILRETPDNILEVQESGEYRCQAQSGPLSSPVHLDFFSSASLILQAPLSVFGDSVV 102

Qy 103 -----ASLILQAPLSVFGDSVVLRCRAKAEVTLNNTIYKNDNVLAFLNKR 149
Db 121 DLITWASQAGITASLILQAPLSVFGDSVVLRCRAKAEVTLNNTIYKNDNVLAFLNKR 180

Qy 150 DFHIFHACLKNGAYRCTGYKESCCPVSSNTVKIQVEPFRPVLRASSFPISGNPVTL 209

181 DBFHIPACILKONGAYRCTGYKESCCPVSSNTVKIQVEPFRPVLRASSQPISENPVTL 240
210 TCETOLSLERSDVLPRFRFRDDOTLGLGWSLSPNFQITAMWSKDSGFYCKAATMPHSV 269
241 TCETOLSLERSDVLPRFRFRDDOTLGLGWSLSPNFQITAMWSKDSGFYCKAATMPHSV 300
270 ISDSPRSITQVQIPASHVPLTSPKALNFGTKVTLHCETOEDSLRLYRFYHGVPLR 329
301 ISDSPRSITQVQIPASHVPLTSPKALNFGTKVTLHCETOEDSLRLYRFYHGVPLR 360
330 HKSVCERGASISFSLTENSNGNYCTADNGLGAKPSKAVSLSVTPVSHVPLNLSSPED 389
361 HKSVCERGASISFSLTENSNGNYCTADNGLGAKPSKAVSLSVTPVSHVPLNLSSPED 420
390 LIPEGAKVTLHCEAQRGSLPILYQPHHEDAALERSANSAGGVAISFSLTAHSGNYCT 449
421 LIPEGAKVTLHCEAQRGSLPILYQPHHEDAALERSANSAGGVAISFSLTAHSGNYCT 480
450 ADNGFGPORSKAVSLSVTPVSHVPLTSSAEALTFEGATVTLHCEVQSGPQILYQFYH 509
481 ADNGFGPORSKAVSLSVTPVSHVPLTSSAEALTFEGATVTLHCEVQSGPQILYQFYH 540
510 EDMLWSSSTPVSIGRVSFSLTEHSGNYCTADNGFGPORSKAVSLSVTPVSHVPLT 569
541 EDMLWSSSTPVSIGRVSFSLTEHSGNYCTADNGFGPORSKAVSLSVTPVSHVPLT 600
570 LRVPRQAQVGDILLEHCEAPRGPPLLYWYFVHEDVTLGSSAPSGEASFNLSLTAHGS 629
601 LRVPRQAQVGDILLEHCEAPRGPPLLYWYFVHEDVTLGSSAPSGEASFNLSLTAHGS 660
630 GNYSCAANGLVAQHSITISLIVPVSRLPILTFRAPRAQVAGDILLEHCEALRGSSPI 689
661 GNYSCAANGLVAQHSITISLIVPVSRLPILTFRAPRAQVAGDILLEHCEALRGSSPI 720
690 LYWFYHEDVTLGKISAPSGGASFNLSLTHSGIYSCADNGLEAQRSEMTLKVA 746
721 LYWFYHEDVTLGKISAPSGGASFNLSLTHSGIYSCADNGLEAQRSEMTLKVA 777

RESULT 13
US-10-040-862-10461
; Sequence 10461, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10461
LENGTH: 592
TYPE: PRT
ORGANISM: Homo sapiens
US-10-040-862-10461
Query Match 57.9%; Score 2962; DB 14; Length 592;
Best Local Similarity 98.6%; Pred. No. 1.1e-198; Indels 4; Gaps 1;
Matches 564; Conservative 0; Mismatches 4
QY 1 MLLWVILLVLAPVSGGFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRFYSPOKTKWHR 60
DB 1 MLLWVILLVLAPVSGGFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRFYSPOKTKWHR 60
QY 61 YLKGKILRETDPNILEVQSGGEYRCQAQSPSSPVHLDSSASLILQAPLSVFEQDSV 120
DB 61 YLKGKILRETDPNILEVQSGGEYRCQAQSPSSPVHLDSSASLILQAPLSVFEQDSV 120
QY 121 LRCAKAEVTLNNTIYKDNVLAFLNKRDFHPIHACLKONGAYRCTGYKESCCPVSSNT 180
DB 121 LRCAKAEVTLNNTIYKDNVLAFLNKRDFHPIHACLKONGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQPPFTRPVLRASSQPIISGNPVTLTCTQLSLERSDVLPRFRFRDDOTLGLWS 240
DB 181 VKIQVQPPFTRPVLRASSQPIISGNPVTLTCTQLSLERSDVLPRFRFRDDOTLGLWS 240
QY 241 LSPNQITAMWSKDSGFYCKAATMPHSVSDSPRSWIOVQIPASHVPLTSPKALNFE 300
DB 241 LSPNQITAMWSKDSGFYCKAATMPHSVSDSPRSWIOVQIPASHVPLTSPKALNFE 300
QY 301 GTKVTLHCETOEDSLRLYRFYHGVPLRHKSVRCERGASISFSLTENSNGNYCTADNG 360
DB 301 GTKVTLHCETOEDSLRLYRFYHGVPLRHKSVRCERGASISFSLTENSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHVPLNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDA 420
DB 361 LGAKPSKAVSLSVTPVSHVPLNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSVTPVSHVPLTSSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSVTPVSHVPLTSSA 480
QY 481 EALTPEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPVSIGRVSFSLTEHSGNY 540
DB 481 EALTPEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPVSIGRVSFSLTEHSGNY 540
QY 541 CTADNGFGPORSSEVVSFLVFT---VPVSRPIL 568
DB 541 CTADNGFGPORSSEVVSFLVFTGKCVLASHPPL 572

RESULT 14
US-10-057-475B-10461
; Sequence 10461, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren

APPLICANT: McNeill, Patricia Dianne
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
FILE REFERENCE: 014058-014402US
CURRENT APPLICATION NUMBER: US/10/057,475B
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 10979
SOFTWARE: Fast-SEQ for Windows Version 3.0
SEQ ID NO 10461
LENGTH: 592
TYPE: PRT
ORGANISM: Homo sapiens
US-10-057-475B-10461

Query Match 57.9%; Score 2962; DB 15; Length 592;
Best Local Similarity 98.6%; Pred. No. 1.1e-198;
Matches 564; Conservative 0; Mismatches 4; Indels 4; Gaps 1;
Qy 1 MLWLVLVLAPVSGQFARTPRPIIFLOPPWTVFOGERVTLTKGFRFYSPOKTKWYHR 60
Db 1 MLWLVLVLAPVSGQFARTPRPIIFLOPPWTVFOGERVTLTKGFRFYSPOKTKWYHR 60
Qy 61 YLGEILRETPDNILVQESGEYRCQAQGSPLSPVHLDPFSSASLIQAPLSVFEGDSVV 120
Db 61 YLGEILRETPDNILVQESGEYRCQAQGSPLSPVHLDPFSSASLIQAPLSVFEGDSVV 120
Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKONGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKONGAYRCTGYKESCCPVSSNT 180
Qy 181 VKIQVQEPFTRPVLRASSFQIPISGNPVTLTCTQLSLERSDVPRLRFRFRDDOTLGLWS 240
Db 181 VKIQVQEPFTRPVLRASSFQIPISGNPVTLTCTQLSLERSDVPRLRFRFRDDOTLGLWS 240
Qy 241 LSPNFQITAMWSKDSGFYKCAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
Db 241 LSPNFQITAMWSKDSGFYKCAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
Qy 301 GTKVTLHCETQBSLRTLRYFYHGVPLRHKSVRCERGAISPSLTTEGSGNYCTADNG 360
Db 301 GTKVTLHCETQBSLRTLRYFYHGVPLRHKSVRCERGAISPSLTTEGSGNYCTADNG 360
Qy 361 LGAKPSKAVSLVTPVSHVNLSSPEDLIFEGAKVTLHCEAQRGSLPLYOFHEDAA 420
Db 361 LGAKPSKAVSLVTPVSHVNLSSPEDLIFEGAKVTLHCEAQRGSLPLYOFHEDAA 420
Qy 421 LERRSANSAGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSIITVPVSHPVLTLSA 480
Db 421 LERRSANSAGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSIITVPVSHPVLTLSA 480
Qy 481 EALTFEATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540

Db 481 EALTFEATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
Qy 541 CTADNGFGPORSVSVSLFVT---VPVSRPIL 568
Db 541 CTADNGFGPORSVSVSLFVTGKCVLASHPPL 572
RESULT 15
US-10-154-884B-10461
Sequence 10461, Application US/10154884B
Publication No. US20040005561A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc W.
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
FILE REFERENCE: 014058-013521US
CURRENT APPLICATION NUMBER: US/10/154,884B
CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 11290
SOFTWARE: Fast-SEQ for Windows Version 3.0
SEQ ID NO 10461
LENGTH: 592
TYPE: PRT
ORGANISM: Homo sapiens
US-10-154-884B-10461

Query Match 57.9%; Score 2962; DB 15; Length 592;
Best Local Similarity 98.6%; Pred. No. 1.1e-198;
Matches 564; Conservative 0; Mismatches 4; Indels 4; Gaps 1;
Qy 1 MLWLVLVLAPVSGQFARTPRPIIFLOPPWTVFOGERVTLTKGFRFYSPOKTKWYHR 60
Db 1 MLWLVLVLAPVSGQFARTPRPIIFLOPPWTVFOGERVTLTKGFRFYSPOKTKWYHR 60
Qy 61 YLGEILRETPDNILVQESGEYRCQAQGSPLSPVHLDPFSSASLIQAPLSVFEGDSVV 120
Db 61 YLGEILRETPDNILVQESGEYRCQAQGSPLSPVHLDPFSSASLIQAPLSVFEGDSVV 120
Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKONGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHPHACLKONGAYRCTGYKESCCPVSSNT 180
Qy 181 VKIQVQEPFTRPVLRASSFQIPISGNPVTLTCTQLSLERSDVPRLRFRFRDDOTLGLWS 240
Db 181 VKIQVQEPFTRPVLRASSFQIPISGNPVTLTCTQLSLERSDVPRLRFRFRDDOTLGLWS 240
Qy 241 LSPNFQITAMWSKDSGFYKCAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300

Thu May 5 15:11:00 2005

Db	241	LSFNFIITAMSKDSGFWCKAATPHSVISDSRSMIQVOIPASHPVLTLSPEKALNFE	300
QY	301	GTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVCRCGASISFSLTTTENSNGNYCTADNG	360
Db	301	GTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVCRCGASISFSLTTTENSNGNYCTADNG	360
QY	361	LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA	420
Db	361	LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA	420
QY	421	LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGQPSKAVSLSVTVPVSHPVLTLSA	480
Db	421	LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGQPSKAVSLSVTVPVSHPVLTLSA	480
QY	481	EALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSPFSFSLTEHSGNYY	540
Db	481	EALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSPFSFSLTEHSGNYY	540
QY	541	CTADNGFGPQSEWVSLFVT---VPSRPIL	568
Db	541	CTADNGFGPQSEWVSLFVTGKCWLASHPPL	572

Search completed: May 4, 2005, 12:01:18
Job time : 106.659 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:24:30 ; Search time 30.6362 Seconds
(without alignments)
3068.392 Million cell updates/sec

Title: US-09-724-254A-41
Perfect score: 5116
Sequence: 1 MLHWVILLVLPVSGQFART.....KVASTVPVSGSLFLASSAPHR 977

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	545.5	10.7	255	2 JC7593	SH2 domain-contain
2	418.5	8.2	344	2 A41357	Pc gamma (IgG) rec
3	418.5	8.2	374	1 A39878	Pc gamma (IgG) rec
4	412	8.1	4351	2 A38096	perlecan precursor
5	402.5	7.9	404	2 A46480	Pc gamma (IgG) rec
6	396	7.7	336	2 I48471	Pc gamma (IgG) rec
7	396	7.7	7962	2 I38346	elastic titin - hu
8	361	7.1	3707	2 S18252	heparan sulfate pr
9	351.5	6.9	738	2 A40096	platelet-endotheli
10	333.5	6.5	847	2 JH0371	B-cell adhesion pr
11	331	6.5	5175	2 T20992	hypothetical prote
12	331	6.5	5198	2 T43290	hemiscitin precurs
13	330	6.5	862	2 I49583	differentiation an
14	330	6.5	1327	2 T09402	immunoglobulin-lik
15	327	6.4	1634	2 S50065	sialoadhesin - mou
16	326.5	6.4	2396	2 I46021	Pc-gamma receptor
17	326	6.4	1896	2 T08851	Down syndrome cell
18	324	6.3	4162	2 T42633	connectin/titin -
19	319	6.2	270	2 A36336	Pc-gamma receptor
20	316.5	6.2	702	2 A36319	carcinoembryonic a
21	312	6.1	868	2 A46512	CD22 homolog/B lym
22	292.5	5.7	254	1 JLO107	Pc gamma (IgG) rec
23	292	5.7	233	1 JU0284	Pc gamma (IgG) rec
24	290	5.7	323	2 S06946	Pc gamma (IgG) rec
25	289	5.6	310	2 JLO119	Pc gamma (IgG) rec
26	287.5	5.6	1070	2 JC4593	protein-tyrosine k
27	286	5.6	3375	2 T19821	hypothetical prote
28	285.5	5.6	1333	2 PN0568	connectin 3B - chi
29	284	5.6	1051	2 A39712	kinase-like protei

telencephalin prec
IgE Fc receptor al
CDO protein - rat
CDO protein - huma
Fc gamma (IgG) rec
Fc gamma (IgG) rec
protein UNC-89 - C
Fc gamma (IgG) rec
Fc gamma (IgG) rec
Fc gamma (IgG) rec
Fc gamma (IgG) rec
Fc gamma (IgG) rec
Fc gamma-1/gamma-2
transmembrane rece
neural cell adhesi
dutt1 protein - mo
protein unc-52 [im

ALIGNMENTS

RESULT 1

JC7593
SH2 domain-containing phosphatase anchor protein 1a - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7593
R;Xu, M.; Zhao, R.; Zhao, Z.J.
Biochem. Biophys. Res. Commun. 280, 768-775, 2001
A;Title: Molecular cloning and characterization of SPAP1, an inhibitory receptor.
A;Reference number: JC7593; MUID:21092675; PMID:11162587
A;Accession: JC7593
A;Molecule type: mRNA
A;Residues: 1-255 <XUA>
A;Cross-references: UNIPROT:Q9BZ16; GB:AF319438
C;Genetics:
A;Gene: spap1a
A;Map position: 1q21
A;Introns: 135/1; 174/1; 183/2; 212/1; 234/1; 243/3
C;Keywords: glycoprotein
F;27-135/Domain: extracellular #status predicted <EXT>
F;68-115/Domain: immunoglobulin-like #status predicted <IGL>
F;148-169/Domain: transmembrane region #status predicted <TMW>
F;195-255/Domain: intracellular #status predicted <INT>

Query Match 10.7%; Score 545.5; DB 2; Length 255;
Best Local Similarity 54.1%; Pred. No. 4.4e-27;
Matches 125; Conservative 27; Mismatches 74; Indels 5; Gaps 4;
QY 731 NGLEAQRSEMT-LKVAVPVSRPVLTRAPGTHAAVGDLLHCEALRGSPILYRPFHE 789
DB 25 NLARHKSFLIAPLCISVPVSRPVLTRSPGAAVGDLLHCEALRGSPILYQFYHE 84
QY 790 DVTGLNRSSPS-GGASLNLSTAEHSGNYSCEADNGLGAQRSTVLYITGLTANRSGPF 848
DB 85 DVTGLNSSAPSGGASFNLSLTAHSGNYSCEANGLGAQCSBAVPVSGPDGYRDLML 144
QY 849 ATGVAGLLSIAGLAGALLCYWLSRKAGRPASDPSPSDSQEPTVYH-VPAWEE 907
DB 145 TAGVLMLGVLGFTGVALLYALFKISGSATNPRGASRNPQEFYYSPTDMEE 204
QY 908 LQPVYNNPRGNVYVSEVRIQEKKAIVASDPRHLRNKSGPIIYSEVK 958
DB 205 LQPVYNNVGSVDVYVSVQWSNQPE--SSANIRTLLENKDSQVIYSSVK 253

RESULT 2

A41357
Fc gamma (IgG) receptor I (high affinity) form b - human
N;Alternate names: CD64
C;Species: Homo sapiens (man)
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004
C;Accession: A41357; S03019

A;Molecule type: mRNA
A;Residues: 1-4391 <MUR>
A;Cross-references: UNIPROT:P98160; CB:M85289; NID:g184426; PIDN:AAAS2700.1; PID:g184427
R;Kallunki, P.; Tryggvason, K.
J. Cell Biol. 116, 559-571, 1992
A;Title: Human basement membrane heparan sulfate proteoglycan core protein: a 467-kD protein with cell adhesion molecules, and epidermal growth factor.
A;Reference number: A41736; PMID:92112994; PMID:1730768
A;Accession: S19256
A;Molecule type: mRNA
A;Residues: 1-57, 'D', '59-434, 'A', '436, 'FL', '438-449, 'Q', '451-502, 'A', '503-792, 'K', '794-908, 'R', '909-919, 'H', '2981-2994, 'G', '2996-3167, 'T', '3169-3240, 'R', '3242-3426, 'R', '3428-3631, 'Q', '3633-3634, 'R', '3635-3636, 'G', '3637-3638, 'T', '3639-3640, 'R', '3641-3642, 'A', '3643-3644, 'R', '3645-3646, 'G', '3647-3648, 'T', '3649-3650, 'R', '3651-3652, 'A', '3653-3654, 'R', '3655-3656, 'G', '3657-3658, 'T', '3659-3660, 'R', '3661-3662, 'A', '3663-3664, 'R', '3665-3666, 'G', '3667-3668, 'T', '3669-3670, 'R', '3671-3672, 'A', '3673-3674, 'R', '3675-3676, 'G', '3677-3678, 'T', '3679-3680, 'R', '3681-3682, 'A', '3683-3684, 'R', '3685-3686, 'G', '3687-3688, 'T', '3689-3690, 'R', '3691-3692, 'A', '3693-3694, 'R', '3695-3696, 'G', '3697-3698, 'T', '3699-3700, 'R', '3701-3702, 'A', '3703-3704, 'R', '3705-3706, 'G', '3707-3708, 'T', '3709-3710, 'R', '3711-3712, 'A', '3713-3714, 'R', '3715-3716, 'G', '3717-3718, 'T', '3719-3720, 'R', '3721-3722, 'A', '3723-3724, 'R', 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C;Keywords: immunoglobulin receptor
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Query Match 7.7%; Score 396; DB 2; Length 336;
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Matches 108; Conservative 43; Mismatches 130; Indels 18; Gaps 12;

QY 3 LWVI--LLVLAIVSGQFARTPRPIIFLOPPWTTVFQGERVLTCTCKGFRFYSQKTKWYHR 60
Db 10 MWLLTLLLVVPGGVVNNKAVITLQPPWASIIQKENVTLWCESGPHLPQDSSQWFIN 69
QY 61 YLQKELRETPD---NILEVQSGEYRCQAQSGPLSSPVHLDFSSAS-LILOAPLSVP-E 115
Db 70 --GTVVQTSPTSPYSISVASFQDSGEYRCQIGSVSPDPVQLQIHKEDWLLQASRRVLTE 127
QY 116 GDSVVLRCRA-KAEVTLNNTIYKNDVLAFLNKRTDFHIPHACLKXNGAYRCTG---YKE 171
Db 128 GEPLALRCHGWNKLVYVNVFVRNGSKFRP-SGSGKIALKTNLSHSGIYHCSGMGRHY 186
QY 172 SCCPVSSNTVKIQVQBPFPTRPVLRASSFQPI-SGNPVTLTCTQLSLERSDVLPRFRPPR 230
Db 187 TSAGVSI-TVKAFPLELFTTPVLRAVSPPFEGSLVTLNCETNLLQRPGLQLYFSFV 245
QY 231 DDQTLGLGWSLSPNQITAMWSKDSGFYCKAATMPSHSVISDSPRSWIOVIP-ASHPV 288
Db 246 GSKILEYR-NTSSEYHIAEREDAGFYMCVATEDSSVLKHPKLEQLQVLGQSSAPV 303

RESULT 7
138346
elastic titin - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: 138346
R;Label: S.; Kolmerer, B.
Science 270, 293-296, 1995
A;Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A;Reference number: A57430; MUID:96026330; PMID:7569978
A;Accession: 138346
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-7962 <RES>
A;Cross-references: UNIPROT:Q10465; EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g1017426
C;Genetics:
A;Gene: GDB:TTN
A;Cross-references: GDB:127867; OMIM:188840
A;Map position: 2q31-2q31

Query Match 7.7%; Score 396; DB 2; Length 7962;
Best Local Similarity 24.2%; Pred. No. 1.1e-15;
Matches 224; Conservative 115; Mismatches 410; Indels 176; Gaps 44;

QY 23 PIIFLOPPWTTVFQGERVLTCTCKGFRFYSQKTKWYHR 69
Db 216 PTFILSRKSLTTFVGKAAKFTCTVTGTPVETIWKDGAALSPSPNWRISDAENKHILEL 275
QY 70 TPDNILEVQSGEYRCQAQSGPLSSPVHLDFSSASLIL-----QAPLSVFEQSV 120
Db 276 SN---LTIQDRGVYSCKA-----SNKFGADLCQELIIDKPHFIKELFVQSAINKKVH 327
QY 121 LRCRA---KAEVTLNNTIYK---NDNVLAFLNKRTDFHIPHACLKXNGAYRCTGYES 172
Db 328 LSCQVDEKVTVTWSKDGKQLPPCKDYKICFEDKIATLEIPKLAKDQSGTYVCTASNEA 387
QY 173 CCFVSSNTVKIQVQBPFPTRPVLRASSFQPI-SGNPVTLTCTQLSLERSDVLPRFRFRDD 232
Db 388 GSSSCSATVTRPEPFSVKV--DPSYLMKPGESARLHCK-----LKGSPV-IQVTFWKN 440
QY 233 QTLGLGWSLSPNF-----QITAMWSKDSGFYCKAATMPSHSVISDSPRSWIOVIPAS 285
Db 441 KEISNTVTRMVFVNSEALDITDKVEDSGSYSCVAV---NDVGSDSCTEIVKEPPS 497
QY 286 HPVLTLSPEKALNFECTKVTILHCT-----QEDSLRT---LYRFYHEGVPLRHK 331

RESULT 5
A46480
Fc gamma (IgG) receptor high affinity - mouse
N;Alternate names: high affinity Igg receptor
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46480; A43511
R;Osman, N.; Kozak, C.A.; McKenzie, I.F.; Hogarth, P.M.
J. Immunol. 148, 1570-1575, 1992
A;Title: Structure and mapping of the gene encoding mouse high affinity Fc gamma RI and
A;Reference number: A46480; MUID:92166399; PMID:1531670
A;Accession: A46480
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-404 <OSM>
A;Cross-references: UNIPROT:P26151
A;Note: sequence extracted from NCBI backbone (NCBIN:85205, NCBIN:85208, NCBIN:85212, NC
R;Sears, D.W.; Osman, N.; Tate, B.; McKenzie, I.F.C.; Hogarth, P.M.
J. Immunol. 144, 371-378, 1990
A;Title: Molecular cloning and expression of the mouse high affinity Fc receptor for IgG
A;Reference number: A43511; MUID:90111035; PMID:2136886
A;Accession: A43511
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-404 <SEA>
A;Cross-references: GB:M31314; NID:G200752; PIDN:AAA40056.1; PID:G200753
C;Superfamily: Fc gamma receptor I; immunoglobulin homology
C;Keywords: immunoglobulin receptor; transmembrane protein
F;127-179/Domain: immunoglobulin homology <IMM>

Query Match 7.9%; Score 402.5; DB 2; Length 404;
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Matches 107; Conservative 42; Mismatches 131; Indels 15; Gaps 10;

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Db 10 MWLLTLLLVVPGGVVNNKAVITLQPPWASIIQKENVTLWCESGPHLPQDSSQWFIN 69
QY 61 YLQKELRETPDNL---EVEQSGEYRCQAQSGPLSSPVHLDFSSASLILQAPLSVP-E 116
Db 70 --GTAVQISPTSPYSIPASQDSGEYRCQIGSSMPSPDVQLQIHNDWLLQASRRVLTEG 127
QY 117 DSVVLRCRA-KAEVTLNNTIYKNDVLAFLNKRTDFHIPHACLKXNGAYRCTGYESCCP 175
Db 128 EPLALRCHGWNKLVYVNVFVRNGSKFQP-SSDSEVAILKTNLSHSGIYHCSGTGRH--R 184
QY 176 VSSNTVKIQVQBPFPTRPVLRASSFQPI-SGNPVTLTCTQLSLERSDVLPRFRFRDDQ 234
Db 185 YTSAGVSI-TVKELFTTPVLRAVSPPFEGSLVTLNCETNLLQRPGLQHLHFSFYVGSKI 244
QY 235 LGLGWSLSPNQITAMWSKDSGFYCKAATMPSHSVISDSPRSWIOVIP-ASHPV 288
Db 245 LEYR-NTSSEYHIAEREDAGFYMCVATEDSSVLKSPSELEQLVGLGQSSAPV 298

RESULT 6
I48471
Fc gamma (IgG) receptor high affinity - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: I48471
R;Prins, J.B.; Todd, J.A.; Rodrigues, N.R.; Ghosh, S.; Hogarth, P.M.; Wicker, L.S.; Gaff
Science 260, 695-698, 1993
A;Title: Linkage on chromosome 3 of autoimmune diabetes and defective Fc receptor for Ig
A;Reference number: I48471; MUID:93242399; PMID:8480181
A;Accession: I48471
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-336 <RES>
A;Cross-references: EMBL:X70980; NID:g311748; PIDN:CAA50311.1; PID:g311749
C;Superfamily: Fc gamma receptor I; immunoglobulin homology

Db 498 F-IKTLBPADIV--RGTNALLQCVSGTGPFEISWFKDKKQIRSSKKYRLFQ-----K 548
Qy 332 SVRCERGASISFSLTITNSGNYCTADNGLCAKPSKAVSLVTPVGHVPLNLSPPDLI 391
Db 549 SLVCLC-----IFSNSADVGVEYCVANVEVKCCMATHL-----LKEPPTFKVVDLI 599
Qy 392 FEGAKVTLHCEAQRGSLPIL-----YQFHEDAALERRSANSAGGVAISF--SLTRAHS 443
Db 600 ALGGQVTLQAAVRGSEPISTVMKQGEVIREDKIKMSFSN---GVAVLIIIPDVQISFG 656
Qy 444 GNYCTADNCGFPQSPKAVSLVTPVSHVPLVTLSSAEAL--TPGATVTLHCEVQRSPQ 502
Db 657 GKYTCLAENAGSQTSGELI-----VKPEAKIIERAELIQVTAGDPATLEYTV--AGTPE 710
Qy 503 ILYOFYHEDPMLWSSSTPSVGRVSF-----SFLTEGH--SGNYCTADNCGFPQSPSEV 554
Db 711 LKPKWYKGRPLVASKK---YRISFKNNVAQLKFSYAEHLHDSGQYTFEISNEVSSCET 767
Qy 555 VSLVTPVVRGPILTLVPRQAQVVGDLLELHCEAPRGSPPIVYFWFHEDVTLGSSAPS 614
Db 768 TFTVLDRIA--PFPTKPLRVNDSVVGTCRLDCKIAGSLPMRVSWF--KD---GKEIAAS 821
Qy 615 G-----GEASFN--LSLTAHSGNYSCEANGLVAQHSDTISLSVIVPVSRIPLTFA 665
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Qy 666 PRAQAVVGDLLELHCEALRGSSPI--LYWFYHEDVTLGKISAPSGG-----ASFNL 715
Db 877 PGKDVLPGSANVCLKSFQSTPTIRWF-----KGNKELVSGGCVYIKEALESLEL 930
Qy 716 SLT--TEHSGIYSCADN---GLEAQRSEMVTLKVAVPVRPVLTLRATPGTHAAVGDLLLEL 771
Db 931 YLVKTSDSGTVCVSNVAGVECS---ANLFVKEPAT--FVEKLEPSQLLKGDATQL 984
Qy 772 HCEALRGSPILYRFHEDVTLGNRSS-----PSGGASLNLIS--LTAHSGNYSCEANGL 825
Db 985 ACK--VTGTPPIKITWFANDREIKESSKHRMSFVESTAVLRLTDVGIEDSGEYMCQAQNEA 1043
Qy 826 GAQRSETVTLVITGLTANRSGPPAT 850
Db 1044 GSDHCSSIVV-----KESPYFT 1061

RESULT 8
S18252
heparan sulfate proteoglycan - mouse
N;Alternate names: perlecan
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 12-Jul-2004
C;Accession: S18252; A31917; B31917; S66460
R;Noonan, D.M.; Fulle, A.; Valente, P.; Cai, S.; Horigan, E.; Sasaki, M.; Yamada, Y.; Ha
J. Biol. Chem. 265, 22939-22947, 1991
A;Title: The complete sequence of perlecan, a basement membrane heparan sulfate proteog
adhesion molecule.
A;Reference number: S18252; MUID:92078153; PMID:1744087
A;Accession: S18252
A;Molecule type: mRNA
A;Residues: 1-3707 <NOO>
R;Cross-references: UNIPROT:Q05793; EMBL:M77174; NID:9200295; PIDN:AAA39911.1; PID:g2002
R;Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogel, G.; Sasaki, M.; Yamada, Y.; Ha
J. Biol. Chem. 263, 16379-16387, 1988
A;Title: Identification of cDNA clones encoding different domains of the basement membra
A;Reference number: A92680; MUID:89034110; PMID:2972708
A;Accession: A31917
A;Molecule type: mRNA
A;Residues: 940-1601 <NO2>
R;Cross-references: GB:J04054; NID:g200252; PIDN:AAA39899.1; PID:g200253
A;Accession: B31917
A;Molecule type: mRNA
A;Residues: 1870-2600 <NO3>
R;Cross-references: GB:J04055; NID:g200300; PIDN:AAA39912.1; PID:g200301
R;Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.

Eur. J. Biochem. 231, 551-556, 1995
A;Title: Structural properties of recombinant domain III-3 of perlecan containing a glob
A;Reference number: S66460; MUID:95377282; PMID:7649154
A;Accession: S66460
A;Molecule type: protein
A;Residues: 1272-1274, X', 1276, X', 1278-1279 <SCH>
C;Keywords: glycoprotein
F;199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;764-811/Domain: laminin-type EGF-like homology <LEG7>
F;1159-1206/Domain: laminin-type EGF-like homology <LEG7>
F;1563-1610/Domain: laminin-type EGF-like homology <EG7>
F;1613-1668/Domain: laminin-type EGF-like homology <LEG8>
F;3163-3198/Domain: EGF homology <EGF>
F;3270-3423/Domain: laminin G repeat homology <LG2>
F;3464-3492/Domain: EGF homology <EGF7>
F;1256,1891,2336,2394,2427/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.1%; Score 361; DB 2; Length 3707;
Best Local Similarity 23.0%; Pred. No. 6.1e-14;
Matches 215; Conservative 108; Mismatches 413; Indels 199; Gaps 45;

Qy 23 PIIFLOPPTVTPQGRVTLTKGFRYPSPQKT-----KWHRYLKGKILRETDPNI 74
Db 1955 PRVQSPERTQVHEGRVRLYCRAGVPSASITWRKEGSLPFRHQHGRSLRL-----HH 2010
Qy 75 LEVQESGEYRCQAQ-----SPLS--SPVHLDFSSALLOAPLS 112
Db 2011 MSVADSGEYVCRANNIDAQETSIMISVSPSTSPAPAPIRIESSS-----R 2062
Qy 113 VFEQSDVLRCAKAEVTLNNTIYKNDNVLAFLNKR--TDFHIPACLKDNKAYRC--- 166
Db 2063 VASGQTLNLCVVPGHAAHQVTHKRGSLPTHQTHGSLRLYQVSSASGEYVCVLS 2122
Qy 167 -TGYSKSCCVSNVTWKIQVQEPFTRPVL--ASSQPISGNPVTLTC-----ETQLSL 217
Db 2123 SSGPLEASVLVSTPAAANVHIPGVVPIRIETSSSRVASEGQTLDLSCVVPQGAHQVTV 2182
Qy 218 ERSDVLPFRFFRDDQTLGLGWSLSPNFOI-----TAMWSKDSGYWCK---AATMP 266
Db 2183 HKR-----GSLPAGHQVGHMLNLRVSPADSGEYSCVGTSSGTL 2255
Qy 267 HSVI-----SDSPRGMVQVIPA---SHPVLTLSPEKALNFEKTKVTLHCETQ--EDSLR 316
Db 2226 ASVLVTIEASESP-----IPAGLAQPVYIESSSHLT--EGQTVDLKCVVPGQAHQ 2277
Qy 317 TLYRFYHGVPLRHKSVRCERGASIS--FSLTTNSGNYCTADNGLGAKPSKAVLSVTV 375
Db 2278 VTHKRGSSLPARHQT-----HGSLLRLYLQSLPADSGEYVCQVAG--SSHPHEASFKLTV 2331
Qy 376 PVSH-----PVLNLSPEDLIFEGAKVTLHCEAQRGSLPILYQPHHDAALERSAN 427
Db 2332 PSSQNSFRILRSPVISIEPPSSVQQQDASFKCLTHEGAMPKIVKWKIRDOELEDNVHI 2391
Qy 428 SAGGVAISF-----SLTAHSGNYYCTADNCGFPQSPKAVSLVTPVSHVPLVTLSSAEAL 483
Db 2392 SPNGSIITIVAPGPATMEPTA---CVASNVYGAQS--VNLNVHGPPT--VSVLPPEGVH 2445
Qy 484 TFEQATVTLHCEVQRGSPQILYFYHEDPMLWSSSTPSVGRVSFSLTSGH----- 535
Db 2446 VKMGKDTILEC--ISSGEPR-----SSPRWRLGIPVKLEPRMFMGLMNSHAMLKIASV 2496
Qy 536 -----SGNYCTADNCGFPQSPSEVVSIFV---TPVSRPILTLRVPRAQAVVGDLLEHCE 588
Db 2497 KPSDAGTYCQAQNALGTAQKQ--VELIVDTGTVAGTPOVQVBESELTLEAGHTATLHCS 2555
Qy 589 APRGSPPIVYFWFHEDVTLGSSAP-----SGCEASFNLSTAHSNGNYSCEANGLVA 642
Db 2556 ATGNPPTTHW-----SKLRAPLPQWHRIGENTLIVPRVAQDQSGQVICHATNS--A 2605
Qy 643 QHSD--TISLSVIVPVSRIPLTFRAPRAQAVVGDLLEHCEALRGSSPIV--WYFHEVDTL 700

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F;340-388/Domain: immunoglobulin homology <IMM1>	
F;424-478/Domain: immunoglobulin homology <IMM2>	
F;602-620/Domain: transmembrane #status predicted <TRA>	
F;621-738/Domain: intracellular #status predicted <CIT>	
F;52,84,151,301,320,344,356,453,467,551/Binding site: carbohydrate (Asn) (covalent) #stat	
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Best Local Similarity 22.6%; Pred. No. 2,7e-14;	
Matches 177; Conservative 120; Mismatches 336; Indels 151; Gaps 33;	
QY 259 WCKAATMPHSVISDSPRSWIQVQIP-----ASHPVILTSPEKAL 297	
DB 5 WAQGATW-----WLGVLTLTLCSLEGQENSFTINSVDMKSLPDTWQNGKNL 53	
QY 298 N---FEGTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVCRCERGASISFLTTE----- 348	
DB 54 TLQCFADVSTTSHVKPOHML-----FYKDDVLV-----YNLSMKSTESFIPE 98	
QY 349 ----NSGNYCYCTADNGLGAKPSKAVSLSVTPVSHVPLNLSPPEDLIFEGAKVTLHCEAQ 404	
DB 99 VRIYDSGYTKCTVIVNNKEXTTAEYQLLVE-GVPSRVTLDKKEAI--QGGIVRVNGSVP 155	
QY 405 RGSPLIYQFH----HEDALERSANSAGVAISFSLTAHSG---NYVCTAD--NGFG 455	
DB 156 EEKAPIHFTIEKLENEKMKVLEKRNKSDONFVLEFPVEQDRLVSLFRCQARIISGIH 215	
QY 456 PQRS---KAVSLSTVPSVSHVPLTLSSAEALTPEGATVTLHCEVQ-----RGSQILYQF 507	
DB 216 MTSSTKSELVTVTESFSPKPHISPT-GNIMEGAQLHIKTIQVTHLAQEPPEII1Q- 273	
QY 508 YHEMPLWSSSTPSVGRVSFSLTEGHSNYYCTANGFGPQSEVSVLFTVTP--VSR 565	
DB 274 --KDKAIVAHNRHGKAVYSVMWVE-HSGNYTKVSS---RISKVSSIVNITELFSK 327	
QY 566 PILTLRVPAQAVVDLLEHCEAPRGSPLIYWFYHEDVTLGSSSAPSGEASFNLSLT 625	
DB 328 PELESSTHLDQ--GERLNLSCSIP-GAPPANFTIQEDTIVSQTQ-----DFTKIAS 377	
QY 626 AEHSGNYSCEANGLVAQHSDTISLSVIVPVSRPILTFRAPRAQAVVDLLEHCEALRG 685	
DB 378 KDSGTIYCTAGIDKVKVKSNTVQIVVCEMLSQPRISYDA-QFVVKGTIETVRCESISG 436	
QY 686 SSPILYWFYHEDVTLGKISAPSGGASFNLSLTHSGIYSCEADN--GLEAQSEWVTL 743	
DB 437 TLPIYSQLLTKTSKVLNENSTKNNDPAVEKNDPTEDVE--YQCVADNCHSHAKMLSEVLRV 494	
QY 744 KVAVPSRPLVTLRAGTHAAVGDLEHCEALRGSPILYRFFHEDVTLGNRSPPSGGA 803	
DB 495 KVIAPVDEVOIISLSKV-VESGEDIVLOCAVNEGSGPITYKYRE-----KEGKFFYOM 548	
QY 804 SLNLS-----LTPAEHSGNYSCEADNGLAQSEVTVLYITGLTANRSGPFGATG 851	
DB 549 TSNAQAFWTKQKASQEGEYCTAFNRANHASSVPRSKILTVRVI-LAPWKGLIAVV 607	
QY 852 VAGGLSTAGLAAGALLYLWLSRKGPK-----PASDPARSPSDSDSOEPTVHNVPAWEE 907	
DB 608 IIGVIALIILIAA-----KCYFLRKAQKQMPVMSRPVPLNLSNNEKMSDPNMEANSH 662	
QY 908 -----LQPVVTNANPRGENVNVSEVRIIOEKKKHVAVPDRHLRKNKSGPIIYSE 956	
DB 663 YGHNDDVRNHAMKPIINDNKEPLNSDVQYTEVQV-----SSAESHKDLGKDKDTETVYSE 715	
QY 957 VKVA 960	
DB 716 VRKA 719	
RESULT 10	
JH0371	
N;Alternate names: B-cell membrane protein CD22	
C;Species: Homo sapiens (man)	

Db 2606 CHTEATVVLHVESP---PYATIPEHTSAQPCNLVQLQCLA-HGTPPLTYQW-----SLV 2656	
QY 701 GKISAPSGGASFNLSL---TTEHSGIYSCEADN--GLEA-----QRSEWVTLKVAVP 748	
Db 2657 GGVLPKAVVRNQLRLLEPTVPEDSGRYRCQVSNRVGSAEFAQVLVQSSSNLPDTSIP 2716	
QY 749 -VSRPVLTLRAGTHAAVGDLEHCEA--LRGSPILYRFFHEDVTLGNRSPPSGGASL 805	
Db 2717 GGSPTVQVTPQLETRNIGASVEFHCAPVNERGTHL---RMLKEGGQLPPGHSVDGVLR 2773	
QY 806 NLSLTAHSGNYSCEADNGLGQORSETVLYITGL 840	
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A;Accession: A40096	
A;Title: platelet-endothelial cell adhesion molecule-1 (CD31) precursor - human	
N;Alternate names: intercellular adhesion protein, carcinoembryonic antigen; leukocyte a	
C;Species: Homo sapiens (man)	
C;Date: 16-Oct-1992 #sequence revision 16-Oct-1992 #text change 09-Jul-2004	
C;Accession: A40096; A48720; JLO142; A43536; A40549	
R;Newman, P.J.; Berndt, M.C.; Gorski, J.; White II, G.C.; Lyman, S.; Paddock, C.; Muller	
Science 247, 1219-1222, 1990	
A;Title: PECAM-1 (CD31) cloning and relation to adhesion molecules of the immunoglobulin	
A;Reference number: A40096; MUID:90193682; PMID:1690453	
A;Accession: A40096	
A;Status: nucleic acid sequence not shown	
A;Molecule type: mRNA	
A;Residues: 1-738 <NEW>	
A;Cross-references: UNIPROT:P16284; GB:M28526; NID:g189775; PIDN:AAA36429.1; PID:g189776	
A;Note: The nucleic acid sequence is shown in reference A40549	
R;Tang, D.G.; Chen, Y.Q.; Newman, P.J.; Shi, L.; Gao, X.; Diglio, C.A.; Honn, K.V.	
J. Biol. Chem. 268, 22883-22894, 1993	
A;Title: Identification of PECAM-1 in solid tumor cells and its potential involvement in	
A;Reference number: A48720; MUID:94043056; PMID:8226797	
A;Accession: A48720	
A;Molecule type: mRNA	
A;Residues: 507-584 <TAN>	
A;Cross-references: GB:S66450; NID:9435845; PIDN:AAB28645.1; PID:g435846	
A;Experimental source: colon adenocarcinoma	
A;Note: sequence extracted from NCB1 backbone (NCBIN:138975, NCBIP:138976)	
R;Simmons, D.L.; Walker, C.; Power, C.; Pigott, R.	
J. Exp. Med. 171, 2147-2152, 1990	
A;Title: Molecular cloning of CD31, a putative intercellular adhesion molecule closely r	
A;Reference number: JLO142; MUID:90278365; PMID:2351935	
A;Accession: JLO142	
A;Status: nucleic acid sequence not shown	
A;Molecule type: mRNA	
A;Residues: 1-7, ADV, 13-213, 1', 215-288, 'E', 290-738 <SIM>	
A;Note: The extracellular domain contains four contiguous C2-like immunoglobulin domains	
R;Stoekinger, H.; Gadd, S.J.; Eher, R.; Majdic, O.; Schreiber, W.; Kasinertk, W.; Straess	
J. Immunol. 145, 3889-3897, 1990	
A;Title: Molecular characterization and functional analysis of the leukocyte surface pro	
A;Reference number: A43536; MUID:91060975; PMID:1700999	
A;Accession: A43536	
A;Molecule type: mRNA	
A;Residues: 1-124, 'V', 126-562, 'N', 564-669, 'G', 671-738 <STO>	
A;Cross-references: GB:M37780; NID:g187239; PIDN:AAA36186.1; PID:g187240	
R;Albelda, S.M.; Muller, W.A.; Buck, C.A.; Newman, P.J.	
J. Cell Biol. 114, 1059-1068, 1991	
A;Title: Molecular and cellular properties of PECAM-1 (endoCAM/CD31): a novel vascular c	
A;Reference number: A40549; MUID:913340830; PMID:1874786	
A;Contents: annotation	
A;Comment: This protein is a widely distributed glycoprotein on endothelial cells, plate	
C;Genetics:	
A;Gene: GDB:PECAM1	
A;Cross-references: GDB:696372	
A;Map position: 17q23-17q23	
C;Keywords: cell adhesion; glycoprotein; phosphoprotein; transmembrane protein	
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384 P-KILPWHAGTYSVAENILGTQORGGAELDVQYPPKVTTVIQNDMPTR-BGDVTVLS 441
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494 CEVQRSGSPQIYQHEDHPLWSSSTPSVG-----RVSFSLTECHSGNYICTADNGFG 548
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442 CNYNSSNPST---RYEWKPHGAWEEPSLGVLKIXQNVGWDNTTIACARCNSWC----- 492
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549 PORSEVVUSLVTPVPSRPILTLY-PRQAQVAGDLELHCLEARPGSPPILYWFPHEDVTL 607
Qy

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608 GSSAFSPGGEASFNL-SLTAEHSGNYSCEANGLVAQHSDTISLSIVTPVPSRPLTLTFRAP 666
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550 -----LGKESQLNFUISPEDAGSVSCVNNSIGQTASKANTLEVLY-APRLRLVMSWP 602
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667 RAQAVVGDDLELHCLEARGSSPILY--WFYHEDVTLGKISAPGGGGASFNL-LTTESHG 723
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603 GDQVMEGKSATLTCS-DAMPVSHVTFWFDNNQSLPHHS-----QKLRLPEVKVQHS 655
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724 IYSCBADNGLBAORSEMVLKVAVPVSRRPVLTLRPGTHAAVGDLELHCLEARGPSLIL 783
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656 AYWCQSTNSVGKRSPSLTV-----677
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784 YRFPHEDVTIGNRSSPSSGASINLSLTABHSGNYSCEADNGLGAORSETVTLTYITGLTAN 843
Qy

678 ---YYSPETIGRAVVLGSCLAIIILA-----IC----GLKLQRWKKTQSQQGLQEN 724
Db

844 RSGPFATGVAGGLLSIAGLAAGALLYCW-----LSRKAGRKPASDPARS--PSDS 894
Qy

725 SSGQ-SFFVRNKVRRAPLSEGPHSLGCYNPMMEDGISYTTLTFPEMNIPTRTGDAESSEM 783
Db

895 QEP-----TY-----HNVPaweeloPYvTWanPRGenvvYSev 927
Qy

784 QRPRPTCDDTVTSALHKRGQVDYENVIPDF-----PEDEGIHYSEL 825
Db

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T20992
 hypothetical protein F15G9.4a - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T20992; T24733
 R:Sulston, J.
 submitted to the EMBL Data Library, December 1994
 A:Reference number: Z19355
 A:Accession: T20992
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-5175 <W12>
 A:Cross-references: UNIPROT:Q8I0L3; EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028
 A:Experimental source: clone F15G9
 R:Kershaw, J.
 submitted to the EMBL Data Library, December 1994
 A:Reference number: Z19929
 A:Accession: T24733
 A:Status: preliminary; translated from GB/EMBL/DDBJ
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 A:Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3;
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 QY 23 PIIFLOPPWTVFGGRVILTCKGFRFYSPQTKYWHRY---LGGKIL-----RTPPDN 73
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A;Status: preliminary; translated from GB/EMBL/DBJ
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A;Residues: 1-5198 <VOG>
A;Cross-references: UNIPROT:O76518; EMBL:AF074901; PIDN:AA26792.1
R;Sulston, J.
Submitted to the EMBL Data Library, December 1994
A;Reference number: Z19355
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A;Status: preliminary; translated from GB/EMBL/DBJ
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A;Residues: 1-5198 <WIL>
A;Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b
A;Experimental source: clone F15G9
R;Kershaw, J.
Submitted to the EMBL Data Library, December 1994
A;Reference number: Z19929
A;Accession: T24734
A;Status: preliminary; translated from GB/EMBL/DBJ
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A;Gene: him-4; F15G9.4b
A;Map position: X
A;Ions: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
A;Ions: 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1;
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Query Match 6.5%; Score 331; DB 2; Length 5198;
Best Local Similarity 22.0%; Pred. No. 7.3e-12;
Matches 200; Conservative 143; Mismatches 398; Indels 170; Gaps 46;

QY 23 PIILOPQWTTVFOGERTVLTCKFRFYSQKTKWHRY---LGKEIL-----RETPDN 73
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QY 74 I-----LEVQSGEYRCQAQGSPLSPVHLDFFSASLILQAPLSVFE-----GDSVV 120
Db 483 VWTIPELSLKDAGEYECRV---ISNNGYSVKTRVETRESPPFIFGVNRVSVPLGEA 538
QY 121 LRC--RAKAEVTLNNTYKNDVLAFLNKRDT-----PHIACLKNDGAYRCTGYKE 171
Db 539 LHCSTRSAGEVIRWTRY---GATVFNQNTERTPTNGTLKIHVTRADAGVIECMA--R 593
QY 172 SCCPVSSNTVKIQOEPFTRPVLRASSFPQISGN---PVLTCETQSLERSDVPLEP-- 226
Db 594 NAGMSTRKMLDIMEP---PSVKVTP-QDVYFNMRGCVNLSCEA-MGDPKPEVHWYFKG 648
QY 227 RFRDDOTLGLGWSLSPNFQITAMWSKDSGFYWCCKAATMPSHVSIDSRSMIQOIPASH 286
Db 649 RHLNDYKYVQGD-SKFLYIRDATHHDEGTGYECRAMSQ-----AGQARDITDML-ATP 701
QY 287 PVLTLSPKALNFEGTKVTLHCETQEDSLRTLYRFYHGVPLRHKS--VRCERGASISFS 344
Db 702 PKVEIIQNMWVGDRVSGFEKTIKRGKPKIRFKNGKDLIKPDDYKINEGQLHMG 761
QY 345 LTTENSGNYCTADNGLGAKPSKAVLSV-TVPVSHPVNLSSPEDL-IFEGAKVTLHC- 401
Db 762 AKDEDAGAYSCVGEN-MAGKDVQVANLSVGRVPTI-----IESPHTVRVNIERQVTLQ 815
QY 402 -----EAQSGSLPILYQPHHEDAALER-RSANSAGGVAISFSLTAHSGNYCTAD 451
Db 816 AVGIPPEIWKQGNVLL-----ATLNNPRYTQADGNLLITDAQIEDQOQFTCIAR 867
QY 452 NGFGPORSKAVLSITVPVSHPVLTLSAAEALTFEGATVTLHCEVQORSQPOLYOFYHED 511
Db 868 NTYG-QOQSOTLLMTVGLVS-PVLGHVPPEEQILIEGQDLTLCVVVLTGTPKPSIWMKDD 925
QY 512 MPMWSSSTPSVGRVSFSFSLTEGH---SGNYCTADNGFGPORSV-VSL-----FVTVP 562
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74 I-----LEVQSGEYRCQAQGSPLSPVHLDFFSASLILQAPLSVFE-----GDSVV 120
Db 483 VWTIPELSLKDAGEYECRV---ISNNGYSVKTRVETRESPPFIFGVNRVSVPLGEA 538
QY 121 LRC--RAKAEVTLNNTYKNDVLAFLNKRDT-----PHIACLKNDGAYRCTGYKE 171
Db 539 LHCSTRSAGEVIRWTRY---GATVFNQNTERTPTNGTLKIHVTRADAGVIECMA--R 593
QY 172 SCCPVSSNTVKIQOEPFTRPVLRASSFPQISGN---PVLTCETQSLERSDVPLEP-- 226
Db 594 NAGMSTRKMLDIMEP---PSVKVTP-QDVYFNMRGCVNLSCEA-MGDPKPEVHWYFKG 648
QY 227 RFRDDOTLGLGWSLSPNFQITAMWSKDSGFYWCCKAATMPSHVSIDSRSMIQOIPASH 286
Db 649 RHLNDYKYVQGD-SKFLYIRDATHHDEGTGYECRAMSQ-----AGQARDITDML-ATP 701
QY 287 PVLTLSPKALNFEGTKVTLHCETQEDSLRTLYRFYHGVPLRHKS--VRCERGASISFS 344
Db 702 PKVEIIQNMWVGDRVSGFEKTIKRGKPKIRFKNGKDLIKPDDYKINEGQLHMG 761
QY 345 LTTENSGNYCTADNGLGAKPSKAVLSV-TVPVSHPVNLSSPEDL-IFEGAKVTLHC- 401
Db 762 AKDEDAGAYSCVGEN-MAGKDVQVANLSVGRVPTI-----IESPHTVRVNIERQVTLQ 815
QY 402 -----EAQSGSLPILYQPHHEDAALER-RSANSAGGVAISFSLTAHSGNYCTAD 451
Db 816 AVGIPPEIWKQGNVLL-----ATLNNPRYTQADGNLLITDAQIEDQOQFTCIAR 867
QY 452 NGFGPORSKAVLSITVPVSHPVLTLSAAEALTFEGATVTLHCEVQORSQPOLYOFYHED 511
Db 868 NTYG-QOQSOTLLMTVGLVS-PVLGHVPPEEQILIEGQDLTLCVVVLTGTPKPSIWMKDD 925
QY 512 MPMWSSSTPSVGRVSFSFSLTEGH---SGNYCTADNGFGPORSV-VSL-----FVTVP 562
Db 926 KPVEEGPTIKIEGGSLLRGNPKDEGKYTCIAVSPAGNSTLHINVLKPKPEVYKP 985
QY 563 -----VSRPIILTRVRAQAVV-----GDLEHCEAPRGPPLIYWFYHEDVTLGSS 610
Db 986 EGGIVPKTTISGMDEKHVAVVNSHVDLDEGFAIFCVWSGTPPTIITWYLD-----GRP 1040
QY 611 SAPSGGASNLSTAE-----HSGNYSCEANGLVAHQSDTISLSVIVPVRP 659
Db 1041 ITPN-----SRDFTVADNTLIVRKADYSYGVVTCQATNSA-----GDNEQKTIIRIMWTP 1092
QY 660 ILTRAPRAQAVVGDLEHCEALRGSSPILYWF-----YHEDVTLGKISAPSGG 709
Db 1093 MISPGQSFMNVVDLFTIPCDVYDGPVITWLLDDKPFTEGVWNEB---GSLTIP--- 1146
QY 710 GASFNLSLTTBHSIGYCEADNGLEAORSEWTLKVAVPVSRPVLTILRAPGTHAAVGDLL 769
Db 1147 -----NVNEAHRGTFTTCAQNA-AGNDTRFVTLVH-----TPTTINAEOKIALQND 1196
QY 770 ELHCEA-LRGSPLILYRFHE- -DVTLCNRSSPGGASLNLSTAEHSGNYCEADNGLG 826
Db 1197 VLECPAKALPPVRLWYVEGEKIDSQILPHITREDGALVLQNVKLENTGVFVQVSN-LA 1255
QY 827 AQRSETVLYI 837
Db 1256 GEDSLSYTLTV 1266
RESULT 12
T43290
hemikent precursor - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43290; T20993; T24734
R;Voegel, B.E.; Hedgercock, E.M.
submitted to the EMBL Data Library, June 1998
A;Description: Hemikent is required for hemidesmosome mediated cell adhesion and germ-
A;Reference number: Z22396
A;Accession: T43290

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Query Match      6.5%; Score 330; DB 2; Length 862;
Best Local Similarity 19.9%; Pred.No.7.5e-13;
Matches 212; Conservative 137; Mismatches 348; Indels 366; Gaps 46;

Qy      3 LWILLVLAVPSGQFA-----RTRPP-----IIFLPQ 29
       |||::: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||: |
Db      6 LWLLILGHAAQAQYSSANDWTVDHPOTLPAWGACIRIPCKYKTLPLPKARLDNILLFQN 65
       |||::: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||: |
Qy     30 PWTTVFOGERVLTICKGFREYSPOKTWKYH-----RYLGKEILRETDPNI-----LEV 77
       |||::: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||: |
Db     66 -----YEFDKATKKFKGTVLNYKAEBELYPKPORRVTFLGNSI-----DNCTLKIHPIRA 115
       |||::: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||: |
Qy    78 QESGE---YRCQAQSPLSPVHLDFGSASL---ILOAPLSVFEGDSVVLCRAKAEVTLAN 133
       |||::: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||: |
Db   116 NDSGNLGLRTAGTHERMEDIHLNVSEKFPQPIQMPSEIRESQSVTLTC-----GLNF. 169
       |||::: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||: |
Qy   134 TIYNKDNLVLAFLNKRTDPhiPHACLKONGAYRCTGYKESCCPVSSNTVKIQOEPTRPV 193
       |||::: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||: |
Db   170 SCEFYDILLQWF-----LEDS---KITSVTPSVTSITS-SVTSSIKNNVYTESK 213
       |||::: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||: |
Qy   194 LRASSFP--ISGNPVTLTCTQLSLERSDVPLAFRRFRDDQTGLGWSLSPNQITAMWS 252
       |||::: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||: |
Db   214 L--TPOPKWTDHGKSVKQVQHSSE-----VLSSERTVRLDVKYVTKPLEI----- 255
       |||::: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||: |
Qy   253 KDSGFYWCKAATPHSVISDSPRSWIQVIPASHPVLTLSPEKALNFEGRKVTLHCETOE 312
       |||::: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||: |
Db   256 -----KNPTEVEKNNSVTMTCRVNSSN 278
       |||::: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||: |
Qy  313 DSIURL-YRFYHEGVPLRHKSVCERGAS--ISFSLJTENSNGNYCYCTADNGLGAKPSKAV 369
       |||::: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||: |

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```

Qy 505 WEELQPP-----VIINAN-----PGENVVIVSRV 527
      : | | | | | | | | | | | | | | | | | |
Db 798 TQAPPPNNSDSVTYSVIQKRPMDGYENVPSCPEDESIHYSFL 840
      : | | | | | | | | | | | | | | | | | |
      : | | | | | | | | | | | | | | | | | |

RESULT 14
T09402
immunoglobulin-like protein IGSF1 - human
C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T09402
R:Mazzarella, R.; Pengu, G.; Jones, J.; Jones, C.; Schlessinger, D.
Genomics 48, 157-162, 1998
A:Title: Cloning and expression of an immunoglobulin superfamily gene (IGSF1)
A:Reference number: 216665; MUID:98190514; PMID:9521868
A:Accession: T09402
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1327 <MAZ>
A:Cross-references: UNIPROT:O15070; EMBL:AF034198; NID:g2645889; PIDN:AAC52057
C:Genetics:
A:Gene: igsf1
A:Map position: Xq25

      Query Match      6.5%; Score 330; DB 2; Length 1327;
      Best Local Similarity 21.8%; Pred. No. 1.3e-12;
      Matches 256; Conservative 159; Mismatches 401; Indels 358; Gaps 61

Qy 13 VSGQFARTPRPIIFLQPPWTTVFGSERVTLTCGK-----PRFYSPQKTKWTHRYLG 63
      : | | | | | | | | | | | | | | | | | |
Db 212 VAGLY--PKPTLTAH--PGPTMAPGESLNLRCQGPYIGWTFALMRVEDLEKS-FYHK--- 263
      : | | | | | | | | | | | | | | | | | |

```

875 RKAGR-----KPSADPARSPSDSDSQ 895
1286 ETDGRDQTALBECNOGEGPT-PANSPSSQSQR 1318
RESULT 15
S50065
sialoadhesin - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S50065
R;Crocker, P.R.; Mucklow, S.; Bouckson, V.; McWilliam, A.; Willis, A.C.; Gordon, S.; Milc
EMBO J. 12, 4490-4503, 1994
A;Title: Sialoadhesin, a macrophage sialic acid binding receptor for haemopoietic cells v
A;Reference number: S50065; MUID:95009950; PMID:7925291
A;Accession: S50065
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1694 <CRO>
A;Cross-references: UNIPROT:Q62230; EMBL:Z36293; NID:g557253; PIDN:CAA85290.1; PID:g55722

Query Match 6.4%; Score 327; DB 2: Length 1694;
Best Local Similarity 20.1%; Pred. NO. 2.9e-12; Indels 410; Gaps 48;
Matches 236; Conservative 125; Mismatches 401;

18 ARTPRPIIPIQPWT-----TVQGERVLTCTCKFRFYSPQKTKWYHR---Y 61
224 AHSRKEVYLOVPHAPKGVILLSSGRNLPDGVTLTCRVNSSYPVAVSQVARDGVN 283
62 LGKEILRETNDILEV-----QSGGEYRQCA---QGSPLSPVHLDPESSASLILQAPLSV 113
284 LG-----VTGHVLRLFSAAMNDGAYTQATNDMGSLSVPLSHLVFMAEVKNNPAGPV 337
114 PEGDSVVLRCRAKAEV--TLNNTIYKNDNVLAFLNKTDFH1PHACLKNGAYRC----- 166
338 LENETVLLCTPKAPQELRYKSWYKHHLEDAHAAT-LHLPAVTRADTGFYFCEVQNA 396
167 -----TGYES-----CCPVSS----- 178
397 QGSRSSPLSVVVRYPPLTDLTLFLEQTAGLVGLHCVVVSEPLATVVLSHGGLTLASN 456
179 -----NTVKIQVOE-----PFTFPLVLA-- 196
457 SGENDFNPRFISSAPNSLRLEIRDLQPADSGEYTCVAVNSLGNSTSSLDPYANVARLLI 516
197 --SSFOIPISGNPVTLTCTQLSLERSDVP-LRFRFRDDQTGLGWSLSPNFOITAMSKD 254
517 NPSAEVVEGQAVTLSCRSGL---SPADTRFSWYLANGALLLEGSSSS--LLLPAASSTD 570
255 SGFTYCKAATPHSVISDSRSPWIOVQIPASHVLT--LSPEKALNFGTKVTTLHCETQE 312
571 AGSYTCRTQAGNTSGPSLP-TVLTFTVYPPKPTFTARLDLDTSGVGGRGILLCHVDS 629
313 D---SIRLTLYRPHGVPLRHKSVCRCGASISFSLTT-----ENSGNYICTADN 359
630 DPPAQLRLHKHVVATSLPSCGSCSQRKTVSRNLSLHVEIQKPVLEDEGVLCESN 689
360 GLGAKPSKAVSLSVTVVSHVPLNLSPEDLIFEGAKVTLHCEAO----- 404
690 TLG-NSSAAAFNAKATVL-----VITPNTLREGTEANLTCNGNOEVAVSPANFSWRN 743
405 -----RGSPLI--LYQFHEDAA-----LERRSANSAGGVAISFSLTAE----- 441
744 GVLMTQGSLETVRLQLLARTDAVYACRLLTEDGQLSAPVLSVLYVADPPKLSALLDV 803
442 ---HSGNYICTADN-----GFGPQR-----SKAVSLSTVPSVHPV 474
804 GQGHMAVFICTVDSYPLAHLSLFRGDHLIATNLEPQPSHGRIQAKATANSIQLEVREL 863
475 LT-----LSSAEALTF-----EGATVTTLHCVQRG-SPQILY 505
864 LVDSGNVHCATNILGSANSLFFQVRGAWVRFTITELREGQAVVLSQCVPTGVSSEGTYS 923

64 KEILRETPDNI-----LEVOESGEYRC-----QAQSPSLSSPVHL---DFSSASLILQAPL 111
264 KTIKNEA--NFFQSLKIQDTGHVLCFYDDASYRGSLLSDVLKIWTDTTPKTKWLLARPS 321
112 SYFE-GDSVVLRCRAKAEVTLNNTIYK--NDNVLAFL-----NKRDTDFH1PHACLKONGA 163
322 AVVQMGQVSLRCRGPDV-GVGLALYKKGEDKPLQFLDATSIDNTTSFFLNNVTVSYDTGI 380
164 YRC---TGKESCCPVSNTVKIQVOEBTPRVLRA---SSFOIPISGNPVTLTCTQLSL 217
381 YSCHYLLTWKTSIRPESHNTVLMVVDKPKFSLSAWPSFTVK--LGKAITLQCRV--- 434
218 ERSVPLRFRFRDQDTGLGWSLSPNFQITAMWSKDSGYWCKAATPHS----- 268
435 --SHPVLEFSLEWEERETQKFSVNGDFIISNVQDKGTGYSCSVRVETHPNWHRSEP 492
269 -----VISDSPR-----SWI----- 278
493 LKLMGPAGYLTWNYVLNEAIRLSLIMQLVALLVVLWIRWKCRRLRIRREAWLLGTAQGV 552
279 -----OVQIPASHPVL-----TLSPEKALNFEKTKVTLHCET 310
553 MLFIVTALLCCGLCNGVLIEETEIVMTPKPELMAETNPPLAPWKNL-----TLWCRS 605
311 QEDSLRTLYRFYHEG--VPLRHKSVCRCGASISFSLTTENSNGNYICTADNGLG-AKPS 366
606 PSGSTKE-FVLLKDGCTGWTATRPASQV-RAAPFLGALTQSTGSHVCHSWEBMAVSEPS 663
367 KAVSLSVTVVSHVPLNLT-----SSPEDLIFE-----G 394
664 EALELGVTDILPKFVISASTIRGOELQRLCKGWLAGMGFALYKEGEQEPVQOLGAVGRE 723
385 -----SSPEDLIFE----- 394
724 AFTTIQRMEDKDEGNVSCRTHTEKRPFKWSEPELELVIKEMYKPFKTKWASPVVTPG 783
395 AKVTLHCEAQRGSLP-ILYQFHEDAAALERRSANSAGGVA--ISFSLTAEHSGNYICT-A 450
784 ARVTFCNSTPHQMSFIVLYKDGSEIASSDRSWASPGASAAHFLIISVIGDGGNYSERY 843
451 DNGFGPORSKAVSLSTVTVSHVPLTSSAEATFEAGATVTLHCEVQRGSPQ-----ILY 505
844 DFSIWSPEPSDELVLVTFEYKPTL-LAQGPVVFVCKSVILRCQ---GTFQGMRRFALLQ 899
506 QFYHEDMPLWSSSTPSVGRVSFSESL-TEG--HSGNYIC---TANGFGPQSRSEVVSFL 558
900 EGAAH--VPL---QFRSVSGNSADFLHTVGAEDSGNYSYCIYYETTMNSRGSYLSMPLMIW 954
559 VTPVSRPILTLRVPRAQAVVDLLELHCEAP-RGSPILYWFYHED-----VTLGSSSA 612
955 VTDTPPKPWL-FAEPSSVPMQNVTLWCGRFVHGVGYIL-----HKEGEATSQWLWGSTS 1009
613 PSGGEASNLSTAEHSGNYSIC---EANNGLVAQHSDTISLSVIVPVSRLPILTFRAPRA 668
1010 NDGAFTTNIGTS--MGRIYCCCHPDPWTSSIKIQPSNTLELLVTGLLPKPSL-LAQGP 1066
669 QAVVGDLLELHCEALRGSSPILYWFYHEDVTLGKI-----SAPSGGASFNL-SL 717
1067 MVAPGENMTLQCC--GSLP-----DSTFVLLKEGAQEPLEQRPSPGYRADFWMPAV 1115
718 TTEHSGIYSC--EADNGLEAQRSEMVTLKVAVPVSRPRLTLRA-PGTHAAVGDILLELHCE 774
1116 RGEDSGIYSCVYLDSTFPAASNSHSDSLIETWTDKPKFSLSAWPSFTMFKGDKITLQCC- 1174
775 ALRGS-PLILYRFFHEDVTLGNRSSPGGASNLSTAEHSGNYSIC-----BADNGLGAQR 829
1175 --RGLPGVEFVLEHDEGAEPQFSEGDGFVIN-NVEKGIGINYSYCSYRLOAYPDWSEP 1231
830 SETVLYITGLTANRSGPFGATG-----VAGLLSIAGLAAGALLCYWL-----S 874
1232 SDFLEL-----VGAAGPVAQCTGVNIVRSSLIIVVVVALGVLAIEKKWPRLTRGS 1285

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:23:49 ; Search time 131.777 Seconds
(without alignments)
3796.562 Million cell updates/sec

Title: US-09-724-254A-41
Perfect score: 5116
Sequence: 1 MLLWVILLVLPVSGGFART.....KVASTPVSGSLFLASSAPHR 977

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	5115	100.0	977	2	Q96RD9
2	2091	40.9	437	2	Q8NF56
3	1563	30.6	734	2	Q96LA4
4	1559	30.5	734	2	Q96P31
5	1559	30.5	742	2	Q8N6S2
6	1549	30.3	740	2	Q96P29
7	1205.5	23.6	639	2	Q96P30
8	1067	20.9	582	2	Q80WN2
9	1067	20.9	595	2	Q68SN8
10	931.5	18.2	508	2	Q96LA5
11	828	16.2	508	2	Q8BUA5
12	826.5	16.2	515	2	Q96RT5
13	820.5	16.0	515	2	Q96RE0
14	772	15.1	360	2	Q8N732
15	714.5	14.0	428	2	Q96P76
16	714	14.0	429	2	Q96LA6
17	651.5	12.7	509	2	Q91YK7
18	645.5	12.6	509	2	Q9EY57
19	628	12.3	366	2	Q8EY59
20	548	10.7	124	2	Q6UY46
21	545.5	10.7	255	2	Q9B216
22	543.5	10.6	154	2	Q8N733
23	537	10.5	343	2	Q8BYS4
24	534.5	10.4	422	2	Q96P73
25	531	10.4	343	2	Q8RAY0
26	529.5	10.3	324	2	Q7TWH2
27	488.5	9.5	722	2	Q6G8N3
28	464.5	9.1	300	2	Q68SP0
29	448.5	8.8	426	2	Q6BAA4
30	446.5	8.7	626	2	Q6DCH3
31	433	8.5	192	2	Q9BZ15

32	430.5	8.4	4071	2	Q6KDZ1
33	428.5	8.4	357	2	Q8SPW5
34	418.5	8.2	374	1	FCG1 HUMAN
35	416	8.1	4391	1	PGBM HUMAN
36	415	8.1	208	2	Q80WN3
37	402.5	7.9	372	2	Q7YQJ5
38	402.5	7.9	404	1	FCG1 MOUSE
39	398.5	7.8	5636	2	Q96RW7
40	397	7.8	144	2	Q9B214
41	396	7.7	330	2	Q8RI42
42	396	7.7	7962	2	Q10465
43	396	7.7	34350	2	Q8W242
44	383	7.5	738	2	P79390
45	375.5	7.3	434	2	Q6DN72

ALIGNMENTS

RESULT 1
Q96RD9 PRELIMINARY; PRT; 977 AA.
AC Q96RD9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE FC receptor-like protein 5.
GN Name=FCRH5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396562; PubMed=11493702; DOI=10.1073/pnas.171308498;
RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;
RT "Identification of a family of FC receptor homologs with preferential
RL Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777(2001).
DR HSSP; P12319; 1F2Q.
GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR SMART; PF00047; Ig; 8.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 8.
KW Receptor.
SQ SEQUENCE. 977 AA; 106496 MW; 24E4A027B25509E7 CRC64;

Query Match	100.0%;	Score	5115;	DB	2;	Length	977;
Best Local Similarity	99.9%;	Pred.	No. 5.2e-315;				
Matches	976;	Conservative	1;	Mismatches	0;	Indels	0;
0;							
QY	1	MLLWVILLVLPVSGGFARTPRPIIFLOPPWTTVFOGERVLTCKGFRFVSPOKTKYHR	60				
Db	1	MLLWVILLVLPVSGGFARTPRPIIFLOPPWTTVFOGERVLTCKGFRFVSPOKTKYHR	60				
QY	61	YLGKELRETDPNILEVQSGEYRCQAQSPVHLPDSSASLILQAPLSVFEQDSVV	120				
Db	61	YLGKELRETDPNILEVQSGEYRCQAQSPVHLPDSSASLILQAPLSVFEQDSVV	120				
QY	121	LRCAKAEVTLNNTIYKNDNLVLAFLNKRITDFHIFHACLDKNGAYRCTGYKESCCPVSSNT	180				
Db	121	LRCAKAEVTLNNTIYKNDNLVLAFLNKRITDFHIFHACLDKNGAYRCTGYKESCCPVSSNT	180				
QY	181	VKIQVEPTRPVLRASSQPIISGNPVTTCTETQLSLERSDVLPRFRFRDDOTLGLWS	240				
Db	181	VKIQVEPTRPVLRASSQPIISGNPVTTCTETQLSLERSDVLPRFRFRDDOTLGLWS	240				
QY	241	LSPNFOITAMWSKDSGFYCKAATMPHSVTSDSRPSWIOVQIIPASHVLTLSPEKALNFE	300				
Db	241	LSPNFOITAMWSKDSGFYCKAATMPHSVTSDSRPSWIOVQIIPASHVLTLSPEKALNFE	300				

301 GTKVTLCETQDSRTLYRFVHEGVPLRHKSVRCERCASISFSITLTSNGNYCTADNG 360
301 GTKVTLCETQDSRTLYRFVHEGVPLRHKSVRCERCASISFSITLTSNGNYCTADNG 360
361 LGAKESKAVSLSVTPVSHVPLNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQPHHEDAA 420
361 LGAKESKAVSLSVTPVSHVPLNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQPHHEDAA 420
421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRKSKAVSLITVPVSHVPLTLSSA 480
421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRKSKAVSLITVPVSHVPLTLSSA 480
481 EALTTEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPVSFVSFSLTEGHSNGNY 540
481 EALTTEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPVSFVSFSLTEGHSNGNY 540
541 CTADNGFGPQRSEVWSLFTVTPVSRPILTRVPRAQAVVGDLELHCEAPRGSPPILYWF 600
541 CTADNGFGPQRSEVWSLFTVTPVSRPILTRVPRAQAVVGDLELHCEAPRGSPPILYWF 600
601 YHEDVTLGSSSAPSGGASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPVSRI 660
601 YHEDVTLGSSSAPSGGASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPVSRI 660
661 LTFRAQAVVGDLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTTE 720
661 LTFRAQAVVGDLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTTE 720
721 HSGIYSCDANGLEAQRSEMTLKVAVPVSRLTLRAPGTHAAVGDLELHCEALRGSP 780
721 HSGIYSCDANGLEAQRSEMTLKVAVPVSRLTLRAPGTHAAVGDLELHCEALRGSP 780
781 LILYRFHEDVTLGNRSSPSGGASLNLSTAEHSGNYSCEADNGLCAQRSETVTLITGL 840
781 LILYRFHEDVTLGNRSSPSGGASLNLSTAEHSGNYSCEADNGLCAQRSETVTLITGL 840
841 TANRSGPFATGAGGLLSIAGLAAGALLYLWLSRKAGRKPSDPSDSQBPPTH 900
841 TANRSGPFATGAGGLLSIAGLAAGALLYLWLSRKAGRKPSDPSDSQBPPTH 900
901 NVPAAEELQPVYTNANPRGENVYSEVRILIQEKKKAVASDPRHLNRKNGSPITVSEVKVA 960
901 NVPAAEELQPVYTNANPRGENVYSEVRILIQEKKKAVASDPRHLNRKNGSPITVSEVKVA 960
961 STPVSGSLFLASSAPHR 977
961 STPVSGSLFLASSAPHR 977

RESULT 2
Q8NF56 PRELIMINARY; PRT; 437 AA.
AC Q8NF56;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-WAR-2004 (TremBLrel. 26, Last annotation update)
DE FLJ00333 protein (Fragment).
GN Name=FLJ00333;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK090423; BAC03404.1; --
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 3.

DR PROSITE; PS00835; IG_LIKE; 3.
FT NON_TER 1_1
SQ SEQUENCE 437 AA; 46521 MW; F56DED36523B52CA CRC64;
Query Match 40.9%; Score 2091; DB 2; Length 437;
Best Local Similarity 99.8%; Pred. No. 4.2e-124;
Matches 404; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 573 PRAQAVVGDLELHCEAPRGSPPILYWFYHEDVTLGSSSAPSGGASFNLSLTAHSGNY 632
DB 33 PGAQAVVGDLELHCEAPRGSPPILYWFYHEDVTLGSSSAPSGGASFNLSLTAHSGNY 92
QY 633 SCANNGLVAQHSDDTISLSVIVPVSRIILTFRAPRAQAVVGDLELHCEALRGSPILYWF 692
DB 93 SCANNGLVAQHSDDTISLSVIVPVSRIILTFRAPRAQAVVGDLELHCEALRGSPILYWF 152
QY 693 FYHEDVTLGKISAPSGGASFNLSLTAHSGNYSCEADNGLCAQRSEMTLKVAVPVSRI 752
DB 153 FYHEDVTLGKISAPSGGASFNLSLTAHSGNYSCEADNGLCAQRSEMTLKVAVPVSRI 212
QY 753 VLTIRAPGTHAAVGDLELHCEALRGSPILYRFHEDVTLGNRSSPSGGASLNLSTAE 812
DB 213 VLTIRAPGTHAAVGDLELHCEALRGSPILYRFHEDVTLGNRSSPSGGASLNLSTAE 272
QY 813 HSGNYSCEADNGLCAQRSETVTLITGLTANRSGPFATGAGGLLSIAGLAAGALLYCW 872
DB 273 HSGNYSCEADNGLCAQRSETVTLITGLTANRSGPFATGAGGLLSIAGLAAGALLYCW 332
QY 873 LSRKAGRKPSDPSDSQBPPTHVNPAAEELQPVYTNANPRGENVYSEVRILIQE 932
DB 333 LSRKAGRKPSDPSDSQBPPTHVNPAAEELQPVYTNANPRGENVYSEVRILIQE 392
QY 933 KKHAVASDPRHLNRKNGSPITVSEVKVASTPVSGSLFLASSAPHR 977
DB 393 KKHAVASDPRHLNRKNGSPITVSEVKVASTPVSGSLFLASSAPHR 437

RESULT 3
Q96LA4 PRELIMINARY; PRT; 734 AA.
AC Q96LA4;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-WAR-2004 (TremBLrel. 26, Last annotation update)
DE Fc receptor-like protein 3.
GN Name=FCRH3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396562; PubMed=11493702; DOI=10.1073/pnas.171308498;
RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;
RT Identification of a family of Fc receptor homologs with preferential B cell expression.;
RL Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777(2001).
DR EMBL; AY043466; AAK91779.1; --
DR HSSP; P12319; 1F2Q.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 6.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 734 AA; 80827 MW; B359B494EBF12138 CRC64;
Query Match 30.6%; Score 1563; DB 2; Length 734;
Best Local Similarity 37.2%; Pred. No. 2.1e-90;
Matches 365; Conservative 94; Mismatches 215; Indels 306; Gaps 13;

Thu May 5 15:11:02 2005

Db 472 PVSREVLTLRAGAAVVDLLEHCELSRFFILYFWFHEDDTLGNISAHSGGASFN 531
 Qy 715 LSLTTHSGIYSCDADNGLEAQRSEMTLVKAVPSRVLTLRAGTHAAVGDLELHCE 774
 Db 532 LSLTT----- 536
 Qy 775 ALRGSPLILYRFHEDVTLGNRSSPGGASLNLSTAEHSGNYSCEADNGLGAQRSETVT 834
 Db 537 -----EHSNGNYSCEADNGLGAQRSHKVT 559
 Qy 835 LYITGLTANRSGPFATGVAGLLSIAGLAAGALLYCWLRSKAGRP----- 881
 Db 560 LNVGTGSRNRTGLTAGITGLVLSILVLAALHLLH---YARARRKPGGLSATGTSSHP 616
 Qy 882 --ASDPARS-PSDSDSQEPTYNVPAWELOPYVTNANPRGENVYSEVRILIQEKKHAY 938
 Db 617 SECQEPSSRRPRIDPQEPHKSPLAPMELEPMYNNVNPDSNPPIYSIQHTKENS 676
 Qy 939 ASDPRHLRNGKSPILYSEVK 958
 Db 677 NCPMTHQEBELTYLSELK 696

RESULT 5

Q8N6S2 Q8N6S2 PRELIMINARY; PRT; 742 AA.
 AC Q8N6S2;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE FCRH3 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer T., Max S.I., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC028933; AAH28933.1; -;
 DR HSSP; P12319; 1F2Q.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig C2.
 DR InterPro; IPR002052; N6_Mtase.
 DR Pfam; PF00047; 19; 4.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG_Like; 6.

DR PROSITE; PS00092; N6_Mtase; UNKNOWN 1.
 SQ SEQUENCE 742 AA; 81853 MW; B0650200E7CA19B8 CRC64;
 Query Match 30.5%; Score 1559; DB 2; Length 742;
 Best Local Similarity 37.1%; Pred. No. 3.9e-90; Indels 306; Gaps 13;
 Matches 364; Conservative 94; Mismatches 216;
 1 MLLWILLVLAVPSQFARTPRPIIFLOPPMTTTFQGERVTLTKGFRFYSPO-KTKWYH 59
 1 MLLWILLVLITPGRQSGVAKAVALLNPNPMTAFKGEKVALICSSISHSIAOQDTWYH 60
 60 RYLKKEILRETPDNILEVOESGEYRCQAGSPSLSPVHLDFSSASLILQAPLSVFGDSV 119
 61 ---DEKLLIKHKDI-QITEPCNYQCKTRGSLSDAVHFEFSPDWLILQALHPVFGDNV 116
 120 VLRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLKONGAYRCTGYKESC---CPV 176
 117 ILRCQKDNKNTHOKVYKDGKQLPNSYNLEKITVNSVSRDNKYHCYAKFYKFLDIEV 176
 177 SSNTVKIQOEPFTRFVLRASSFQIPISGNVTLTCTETQSLERSDPLRFFRDDDTLG 236
 177 TSKPINIQVELFHPVLRASSSTPIEGSPMTLTCTETQSPQPDVQLOFLRDSQTLG 236
 237 LGWSLSPNFOITAMSKDSGFYWCRAATMPHPSVISDSPRSMTQVOIPASHVPLTLSPEKA 296
 237 LGWSRSPRLQIPAMWTEDSGSYWCEVETVTHSIKRSLSRQIRVO----- 281
 297 LNFEGTKVTLHCETQDSLRTLRYFYHGVPLRHKSVCRCERGASISFSLTENSNGYCT 356
 282 ----- 281
 357 ADNGLGAKPSKAVSLSVTVPSHPVLNLSPEDLIFEGAKVTLHCEAORGSLPIYQPHH 416
 282 -----RVPSNVNLEIRPTGQGLIEGENWVLICSAVQSGSTVTFSMHK 324
 417 ED--AALERSANSAGGVAISFSLTAHSGNYYCTADNGFGPORSKAVLSITVPVSHVY 474
 325 EGRVRSRQKLT-----QRSLAEHL-----V 345
 475 LTLSSAALTFEGATVTLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSPFSILTEG 534
 346 LTVKESDA----- 353
 535 HSGNYYCTADNGFGPORSSEVSVLFTVTVPSRPIITLVRPRAQAVVGDLELHCEAPRGSP 594
 354 --GRYCAADNVHSPILSTWIRTVIPVSHPLTFRAPRAHTVVGDLLEHCELSRGSP 411
 595 PLYWYFYHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANNGVAQSHDTSLSIV 654
 412 PLYRIFYHEDVTLGSSAPSGGASFNLSLTAHSGNYSCEADNGLGAQRSHGVSLRTV 471
 655 PVSRLITFRAPRAQAVVGDLELHCEALRGSSPIYWFYHEDVTLGKISAPSGGGASFN 714
 472 PVSRLITFRAPRAQAVVGDLELHCELSRGSPPIYWFYHEDDTLGNISAHSGGASFN 531
 715 LSLTTHSGIYSCDADNGLEAQRSEMTLVKAVPSRVLTLRAGTHAAVGDLELHCE 774
 532 LSLTT----- 536
 775 ALRGSPLILYRFHEDVTLGNRSSPGGASLNLSTAEHSGNYSCEADNGLGAQRSETVT 834
 537 -----EHSNGNYSCEADNGLGAQRSHKVT 559
 835 LYITGLTANRSGPFATGVAGLLSIAGLAAGALLYCWLRSKAGRP----- 881
 560 LNVGTGSRNRTGLTAGITGLVLSILVLAALHLLH---YARARRKPGGLSATGTSSHP 616
 882 --ASDPARS-PSDSDSQEPTYNVPAWELOPYVTNANPRGENVYSEVRILIQEKKHAY 938
 617 SECQEPSSRRPRIDPQEPHKSPLAPMELEPMYNNVNPDSNPPIYSIQHTKENS 676
 939 ASDPRHLRNGKSPILYSEVK 958

Qy	589	APRGSPILYWFYHEDVTLTGSSAPSGGEASFNLSTAEHSGNYSCEANNGLVQAHS	DTI	648
Db	412	SLRGSPLLRYFYHEDVTLGNSSAPSGGGASFNLSTAEHSGNYSCEADNGLGAQ	HSHV	471
Qy	649	SLSVIVPVSRIITFRAPRAQAVVDLLELHCEALRGSSPLLRYFYHEDVTLGKIS	APSG	708
Db	472	SLRVTVPVSRIITLAPGAQAVVDLLELHCESLRGSFPILRYFYHEDDVLGNI	SAHSG	531
Qy	709	GGASFNLSTAEHSGIYSCADNGLEAQRSEMTLVKAVPVSRPVLTLRAPGTHAA	VGLD	768
Db	532	GGASFNLSTAEHSGIYSCADNGLEAQRSEMTLVKAVPVSRPVLTLRAPGTHAA	VGLD	768
Qy	769	LELHCEALRGSPILRYFYHEDVTLGNRSSPSSGGASLNLSTAEHSGNYSCEADNGL	GAQ	828
Db	543	LELHCEALRGSPILRYFYHEDVTLGNRSSPSSGGASLNLSTAEHSGNYSCEADNGL	GAQ	559
Qy	829	RSTVTILYITGLTANRSGPPATGVAGLLLSIAGLAAGALLYCWLSSKAGRP		881
Db	560	HSKVVTLNVTGTSRRNTGLTAAGITGLVLSILVLAALH---	YARARRKPGGLSATG	616
Qy	882	-----ASDPARS-PSDSDSOEPTVHNVPAMEELQPVVTNPRGENVVYSEVRI	IQE	932
Db	617	TSHSPSECOEPPSSRRSDPOEPHTSKPLAPMELEPMYSNVNPGDSNP	PIYSQIWSIQH	676
Qy	933	KKGHAVASDPRHLNRKSGPIIYSEVK	958	
Db	677	TKENSANCPMMHQEHELTVLYSELK	702	

RESULT 7

Q96P30 PRELIMINARY; PRT; 639 AA.

ID Q96P30 PRELIMINARY; PRT; 639 AA.

AC Q96P30; 01-DEC-2001 (T-EMBLrel. 19, Created)

DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)

DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)

DE SH2 domain-containing phosphatase anchor protein 2b.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_Taxid:9606;

RN [1] SEQUENCE FROM N.A.

RP Xu M.-J., Zhao R., Zhao Z.-J.;

RA Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF416902; AAU13291.1; -;

DR HSSP; P12319; 1F2Q.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig c2.

DR InterPro; IPR002052; N6_Mtase.

DR Pfam; PF00047; Ig; 3.

DR SMART; SM00408; IGC2; 1.

DR PROSITE; PS50835; IG_LIKE; 5.

DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.

SQ SEQUENCE 639 AA; 59928 MW; 6927ADAE64CA984 CRC64;

Query Match 23.6%; Score 1205.5; DB 2; Length 639;

Best Local Similarity 31.2%; Pred. No. 7.5e-68;

Matches 305; Conservative 85; Mismatches 192; Indels 395; Gaps 14;

Qy	1	MLLWLVLLVAPVSGOFARTPRPIFLQPPWTVFQGERVTLTCCKGFRFYSPO-KTKWYH	59
Db	1	MLLWLVLLVTPREGSGVNPAPKAVLLNPNPWFSTAFKGEKVALICSSISHSLAQODT	60
Qy	60	RYLGKEILRETDPNILEVOESGEYRCQAQSGPLSPVHLDFSSASLILOAPLSYFEGDSV	119
Db	61	---DEKLLKIKHDKI-QITEPGNYQCKTRCSSLSDAVHVEFSPDWLLILQALHPVEGDV	116
Qy	120	VLRCKAEAVTLNNTYIKQDNVLAFLNKRTDFHHPHACLKDNQAYRCTLGKSCCPVSSN	179
Db	117	ILRCQGDKNKNTHQKVYKDGKQLPNSYNLEKITVNSVRSDNKKYHCTAYRK-----	168

submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.

EMBL; AY158090; AAC20873.1; -.
HSP; P12319; IF2Q.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
Pfam; PF00047; Ig_3.
SMART; SM00408; IGC2; 2.
PROSITE; PS50835; IG_LIKE; 5.
SEQUENCE 582 AA; 65248 MW; 44321E93FE9EDF06 CRC64;

[illegible]

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QY 893 DSQEPYHNVPAMELOPVTYNNPRGENVYSEVRIIOEKKKHA 937
DQ 893 :||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 523 EPOEPTYNNPACIELOPVYSN-EPE-ENVIYEVRRTPQKHA 565
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 9
Q68SN8 PRELIMINARY; PRT; 595 AA.
AC Q68SN8
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE FC receptor-like protein 3.
GN Name=FcRh3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Spleen;
RA PubMed=15302849;
RX Davis R.S., Stephan R.P., Chen C.C., Dennis G. Jr., Cooper M.D.;
RT "Differential B cell expression of mouse fc receptor homologs.";
RL Int. Immunol. 16:1343-1353(2004).
DR EMBL; AY065558; AAS91578.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003595; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; IGC2; 4.
DR SMART; SM00408; IGC2; 4.
DR PROSITE; PS50835; IG_LIKE; 5.
KW Receptor.
SQ SEQUENCE. 595 AA; 66619 MW; 6AEDB8E2F6AFACF CRC64;

Query Match 20.9%; Score 1067; DB 2; Length 595;
Best Local Similarity 29.8%; Pred. No. 4e-59;
Matches 282; Conservative 82; Mismatches 191; Indels 390; Gaps 15;

QY 3 LWILLVLAPVSGFARTPRPIPLQPPWTVFQGERVTVTCGFRPYSPQKTKWYHYL 62
Db 14 MWLLTLVTPVNGQHEAAQSVLSQPPWTVFQGERVTVTCGFRPYSPQKTKWYHYL 71
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 63 GKILRETPD-----NILEVQSGEYRCQAQSPVLDPSASLILQAPLSVPEG 116
Db 72 -RTVVTQTPGALVKAHTLVKHSGEYWCQADSLPSMHVNVFESEDFVLQAPPVFE 130
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 117 DSVVLRCAKAEVTLNN-TYKNDNVLAFLNKRDTDFHIFACLDKNGAYRCTGYKESC-- 173
Db 131 DSVVLRCAKAEVTLNN-TYKNDNVLAFLNKRDTDFHIFACLDKNGAYRCTGYKESC-- 173
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 174 CPVSSNTVKIQOEPFTRPVLRASSFQIPISGNPVITCTQSLERSDVLPRFRFRDDQ 233
Db 190 SLYTSNTVGVQVQELFPRPVLRASSFQIPISGNPVITCTQSLERSDVLPRFRFRDDQ 249
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:
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      :||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 234 TLGLGWSLSPFOITAMWSKDSFGYCKATMPSHVISDSFSPWIOVQIPASHPVLTSP 293
Db 250 LLGGGCSRSSEFHPAIWTBESRRYQCAETVNSQVRKQSTAFIIPVQ----- 297
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:
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      :||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 294 EKALNPEGTKVTLHCETQEDSLRTLRFYHEGVPLRHKSVRCERGASISFSLTENS 353
Db 298 -----RASARFQTHIP----- 309
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 354 YCTADNGLGAKPSKAVSLSVTPVSPHVLNLSPEDLIFEGAKVTLHCEAQRGLPILYQ 413
Db 310 ----- 309

QY 414 FHEDAALERRSANSAGGVAISFLTAHSGNCTYCTADNFGFGPQRSKAVSLSVTPV 473
Db 310 ----- 309
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DR Genew; HGNC:14875; SPAP1.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 3.
DR PROSITE; PS00835; IG_LIKE; 3.
KW Receptor.
SQ SEQUENCE 508 AA; 55541 MW; 9AB30E0411B41EDC CRC64;

Query Match 18.2%; Score 931.5; DB 2; Length 508;
Best Local Similarity 29.6%; Pred. No. 1.2e-50; Gaps 13;
Matches 254; Conservative 69; Mismatches 161; Indels 375;

QY 104 SLIIQAPLSVFGDSVWLRCRAKAEVTLNNITYKNDN-VLAFLNKRTPDHPHACLKDNG 162
DB 19 SLITLAPSSVFGDSVILVKCGEQNKWKQAYHKDKLSVFKFDFLIQSAVLSDSG 78

QY 163 AYRC-TGYKESCCPVSSNTVKIQVQEPFTRPVLRASSQPTSGNPVTITCTOISLERSD 221
DB 79 NYFCSTKGQLFLWDKTSNIVKIKVQELFORPVLTAASSQPIEGGPVSLKCTETRLSPQLD 138

QY 222 VPLRPFRRDDTLGLGWSLSPNFQITAMWSKDSGFYWCKAATMPHVSIDSPSRWIQVQ 281
DB 139 VOLQCFRRNQVLGGWSSSELQLSAVWSEDTGSYWCKAETVTHIRKQSLQSIHQV 198

QY 282 IPASHPVLTLSPEKALNFEGTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCRCGASI 341
DB 199 ----- 198

QY 342 SFLSTTENGNYCTADNGLGAKPKSAVSLVTPVSHVPLNLSSPEDLIFEGAKVTLHC 401
DB 199 ----- RIPSNVSLERAPGGQVTEGQKLLILC 226

QY 402 EAQSGSLPILYQFHEDHAALERRSANSAGGVA-ISFSLTAHSGNYCTADNGFGPQSK 460
DB 227 SV-----ACGTGNVTFSWYREATG-----TSMGKKTOR 254

QY 461 AVLSITVPVSHVPLTLSSAELTFEGATVTLHCEVQSGSPQILYQFYHEDPLWSSPT 520
DB 255 SLSAELSLP----- 263

QY 521 SVGRVSFSLTECHSGNYCTADNGFGPQSEVSLFTVPVSRPILTLRVPRAQAVVG 580
DB 264 -----AVKESDAGKYCRADNGHVPICQKVNIPVSRPVLTLRSPGAQAVG 314

QY 581 DLLELHCEALRGSPILYQFYHEDVTLGSSAPSGGEAFNLISLTAHSGNYSCAANNGL 640
DB 315 DLLELHCEALRGSPILYQFYHEDVTLGNSAPSGGASFNLSLTAHSGNYSCAANNGL 374

QY 641 VAQSDTISLSVIVPVSRLPILTPRAPAAQAVGDLLELHCEALRGSSPILYQFYHEDVTL 700
DB 375 GAQCSEA-----VPVS----- 385

QY 701 GKISAPSGGASFNLSLTAHSGNYSCAANNGLVAQSEWTLKAVPVSRLPILTRAPG 760
DB 386 -----ISGPDG-----YRDLMT----- 398

QY 761 THAAVGDLELHCEALRGSPILYQFYHEDVTLGNRSSPGSGASLNLSLTAHSGNYSC 820
DB 399 ----- 398

QY 821 ADNGLGAQRSEITVLYITGLTANRSGPPATGVAGGLLSIAGLAAGALLYCWLSRKAGR 880
DB 399 -----AGVLCGLFGVLGFTGVALLLYALPFLKISGES 429

QY 881 PASDPARPSDSQSEPTVHN-VPABELOPYTNANRGENVVYSEVRIITQEKKHAVA 939
DB 430 SATNEPRGASRNPQSEFTYSSTPDMELQPYVNVGSDVDVYVSQVMSQQPE---SSA 487

QY 940 SDPRHLRNKGSPIIYSEVK 958
DB 488 NIRTLENNKDSQVITYSSVK 506
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GN Name=FCRH4;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RX SEQUENCE FROM N.A.
RP MEDLINE=21396562; PubMed=11493702; DOI=10.1073/pnas.171308498;
RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;
RT "Identification of a family of Fc receptor homologs with preferential
RT B cell expression."
RT Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777 (2001).
DR EMBL; AF397452; AK93970.1; -.
DR HSSP; P12319; IF2Q.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
KW Receptor.
FT NON_TER 1 360
SQ SEQUENCE 360 AA; 57250 MW; 32FBD6FAB2B19D3D CRC64;

Query Match 16.0%; Score 820.5; DB 2; Length 515;
Best Local Similarity 43.3%; Pred. No. 1.3e-43;
Matches 183; Conservative 55; Mismatches 162; Indels 23; Gaps 6;

QY 1 MLLWVILLVLPVSGOPARTPRPIIFLOPPWTVFOGERVTLTCKGFYSPQTKWYHR 60
DB 1 MLLWASLLAFVCGQAAAHKPVISVHPWTVTFKGERVTLTCKGFYATEKTWYHR 60
QY 61 YLGEKILRETPDNILEVOESGEYRQAGSPLSPVHLDFSSASLLILOAPLSVFEQSVV 120
DB 61 HYWGEKLTLPFGNTLVRESGLYRCQARGSPRNPVRLFFSSDSLLILOAPYSVFEQDTLV 120
QY 121 LRCRAKAEVTLNNTIYK-NDNVLAFLNKRDTDFHACLDKNGAYRCTGYKESCCPVSSN 179
DB 121 LRCHRRRKEKLTAVKYTWNGNLSISNKSDDLIPQASSNNNGYRCIGYGDENDVFRLN 180
QY 180 TVKIQVOEPFTRPVLRASSFOPIISGNFVTLTCTQSLERSDVPFRFRDDQTLGLW 239
DB 181 FKIKIQELFPHPELKATDSQPTGNSVNLSCETQLPERSDTPLFHNFRRDGEVILSDW 240
QY 240 SLSPNFQITAMWSKDSGYWCAATMPSHVSIDSPRSWIOVO-IPASHPVLTLSPEKALN 298
DB 241 STYPELQPTVWRENSGSGYWGAEVTRGNHHKSPSLQIHVQIPVSGVILLETQPSGQA 300
QY 299 EGTGKVTLLHCTQEDSLRTLYRFYHEGV--PLRHKSVCRCGASISFSLTTSNGNYCT 356
DB 301 VEGEMLVLCVSAEGTGTTFSHREDMQESLGRKTSRLRAELPAIRQSHAGGYCT 360
QY 357 ADNGLGAKPSKAVSLVTVVPSVHPVNLVSSPEDLIFEGA-----KVTLHCEAQ 404
DB 361 ADNLSYG--PVQSMVLNVTRETP-----GNRDGLVAAGATGGLLSALLLAVALLFHCWRR 413
QY 405 RCS 407
DB 414 RKS 416

RESULT 14
Q8N732 PRELIMINARY; PRT; 360 AA.
ID Q8N732
AC Q8N732;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE D3801G22.1 (Novel immunoglobulin domain protein similar to
DE immunoglobulin receptors) (Fragment).
OS Names=DJ801G22.1;
GN Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RX SEQUENCE FROM N.A.
RP Bagguley C.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AL135929; CAB92753.1; -.
DR HSSP; P12319; IF2Q.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
KW Receptor.
FT NON_TER 1 360
SQ SEQUENCE 360 AA; 40724 MW; 7ACC2E7FA3256D62 CRC64;

Query Match 15.1%; Score 772; DB 2; Length 360;
Best Local Similarity 46.1%; Pred. No. 9.5e-41;
Matches 165; Conservative 49; Mismatches 138; Indels 6; Gaps 4;

QY 22 RPIFLQPPWTVFOGERVTLTCKGFYSPQTKWYHYLKGKILRETPDNILEVOESG 81
DB 4 KPVISVHPWTVTFKGERVTLTCKGFYATEKTWYHRYGKELTLPFGNTLVRESG 63
QY 82 EYRCQAQGSPLSPVHLDFSSASLLILOAPLSVFEQSVVLRCAKAEVTLNNTIYK-NDN 140
DB 64 LYRCQAQGSFRNPVRLFFSSDSLLILOAPYSVFEQDTLVLRCHRRRKEKLTAVKYTWNGN 123
QY 141 VLAFLNKRDTDFHACLDKNGAYRCTGYKESCCPVSSNTVKIQVOEPFTRPVLRASSFQ 200
DB 124 ILSISNKSDDLIPQASSNNNGYRCIGYGDENDVFRSFKIKIQELFPHPELKATDSQ 183
QY 201 PISGNPVTLTCTQSLERSDVPFRFRDDQTLGLGWSLSPNFQITAMWSKDSGYWCA 260
DB 194 PTEGNSVNLSCETQLPERSDTPLFHNFRRDGEVILSDWSTYPELQPTVWRENSGSGY 243
QY 261 KAATMPSHVSIDSPRSWIOVO-IPASHPVLTLSPEKALNFEQTKVTLHCTQEDSLRTLY 319
DB 244 GAETVRGNHHKSPSLQIHVQIPVSGVILLETQPSGQAVEGEMLVLCVSAEGTGTTF 303
QY 320 RPYHEGV--PLRHKSVCRCGASISFSLTTSNGNYCTADNGLGAKPSKAVSLSVTV 375
DB 304 SHREDMQESLGRKTSRLRAELPAIRQSHAGGYCTADNSYG--PVQSMVLNVTV 359

RESULT 15
Q96PJ6 PRELIMINARY; PRT; 428 AA.
ID Q96PJ6
AC Q96PJ6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE IFGP1.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX SEQUENCE FROM N.A.
RP MEDLINE=22033006; PubMed=12037601; DOI=10.1007/s00251-002-0436-x;
RA Guselnikov S.V., Ershova S.A., Mechetina L.V., Najakshin A.M.,
RA Volkova O.Y., Alabyev B.Y., Taranin A.V.;
RT "A family of highly diverse human and mouse genes structurally links
RT leukocyte FcR, gp42 and PECAM-1."
RT Immunogenetics 54:87-95 (2002).
RL EMBL; AF329488; AAL23898.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 3.
DR PROSITE; PS50835; IG_LIKE; 3.

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SQ	SEQUENCE	428 AA; 46865 MW; F20BA31110BBC7828 CRC64;	Query Match Best Local Similarity Matches 207; Conservative 45; Mismatches 152; Indels 373; Gaps 9
Qy	188	PFTRPV---LRASSFQPIGSPVTLTCTQTSLERSDVPLFRFRDDQTGLGNSLSPN	244
Db	12	PLCEPABLFLLIASSHPHTEGSPVTLTKMPF-LQSSDAQFOCFRFRDTRALGPGWSSPK	70
Qy	245	FQITAMSKDSGFYCKCAATPHSVISDSPRSWIQVQIPASHPVLTLSPKALNPEGTKV	304
Db	71	LQIAAMNKBDTGSYWCBAQTMAKVLK-SRSQINV-----	105
Qy	305	TLHCETOEDSLRTLYRFHYEGVPLRHKSVRCERGASISFSLTTENSGNYCTADNGLGAK	366
Db	106	-----HR-----	107
Qy	365	PSKAVLSLTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAALERR	424
Db	108	-----VPVADVSLTQPPGGQVMEGRDLVLI CSVANGTGDITFLWKYGAVLNLQ	157
Qy	425	SANSAGGVAISFSLTAEHSGNYCTADNGFGQRKAVSLSI TVPVSHPVLTLSAEALT	484
Db	158	SKTOR-----SLTAEY-----	168
Qy	485	FEGATVTLHCEVQRGSQILYQFYHEDMPLWSSSTPVSGRVSPFSLTEHSGNYCYCTAD	544
Db	169	-----BIP-----SVRESDAEQYVCAE	186
Qy	545	NGRGPQRSEVVSLPVTVPVSRPILTLRVPRAAQVVGDLLELHCEAPRGSPPILYWFYHED	604
Db	187	NGYGPSFGLVSI TVIPVSRPILMLRAPQAQAVEDVLELHCEALRGSPPILYWFYHED	246
Qy	605	VTLGSSAPSGGGEASFNLSTAEHSGNYSCANNGLVAQHSDTISLSVIVPVSRIPLTFR	664
Db	247	ITLGRSAPSGGGASFNLSTEEHSGNYSCAN-----	279
Qy	665	APRAQA VVGDLLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGGASFNLSTTEHSGI	724
Db	280	-----	279
Qy	725	YSCEADNGLQAQRSEMVTLKVAVPVSRPVLTLRAPGTHAAVGDLELHCEALRGSPILTY	784
Db	280	-----	279
Qy	785	RPFHEDVTLGNRSSPSGGASINLSLTAHSGNYSCADNGLGAQRSETVTLTYITGLTANR	844
Db	280	-----NLGAQRSEAVTLNFTVPTGAR	301
Qy	845	SGPFATGVAGGLLSIAGLAAGALLYCWLSRKAGRKCPASDPARSPSDSDSQEPTVHNVA	904
Db	302	SNHLTSGVIEGSLTLGPAIVALLFCYGLKRGKIGRRSARDPLRSLPPLPQEFYLYNSPT	361
Qy	905	WEELOPVYTANPGENVNVTVSEVRIIQKKKHAVASDPRLHNRKSGPIIYSEKVAS	961
Db	362	PGLOQPTIENNVVSGDEVTSLAYNGPQESVAETLGTHTMEDKVSLDIYGLRLKAN	418

Search completed: May 4, 2005, 11:38:08
Job time : 139.777 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:20:49 ; Search time 97.8093 Seconds
(without alignments)
3001.261 Million cell updates/sec

Title: US-09-724-254A-44
Perfect score: 3993
Sequence: 1 MLWVILLVLAPVSGQFART.....MVLKVGAEWALPTSSTSEN 759

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3993	100.0	759	4	AAB82313
2	3993	100.0	759	7	ADM35235
3	3923	98.2	977	4	AAB82315
4	3923	98.2	977	7	ADM35237
5	3916	98.1	977	6	ABP97215
6	3720	93.2	875	8	ABM82476
7	3487	87.3	837	8	ABM82477
8	2962	74.2	592	7	ADM35236
9	2962	74.2	592	6	ABU99155
10	1419.5	35.5	582	6	ADM35238
11	1419.5	35.5	582	7	ADM35239
12	1417.5	35.5	707	7	ADM35237
13	1417.5	35.5	734	4	AAB82316
14	1417.5	35.5	734	7	ADM35238
15	1417.5	35.5	750	8	ABM84916
16	1415	35.4	733	8	ADL06557
17	1400	35.1	727	6	ABP84668
18	1374.5	34.4	554	7	ADF74336
19	1374.5	34.4	717	7	ADF74337
20	1374.5	34.4	717	7	ADF74318
21	1287.5	32.2	718	8	ABM84917
22	1255	31.4	707	8	ABM84918
23	1120	28.0	222	5	ABP69283
24	1064	26.6	639	7	ADJ70604
25	1064	26.6	655	8	ABM84920

26	1012.5	25.4	641	8	ABM84919	Abm84919 Human dia
27	900	22.5	181	5	ABP51264	Abp51264 Human MDD
28	900	22.5	181	5	ABP51409	Abp51409 Human MDD
29	889.5	22.3	570	7	ADF74389	Adf74389 Murine FC
30	889	22.3	468	7	ADF74391	Adf74391 Extracell
31	884.5	22.2	327	5	ABP63021	Abp63021 Human pol
32	883	22.1	470	7	ADL22727	Adl22727 Human dis
33	871.5	21.8	421	6	ABU99156	Abu99156 Novel hum
34	871.5	21.8	421	6	ABU99157	Abu99157 Novel hum
35	871.5	21.8	421	8	ADM93877	Adm93877 Human NOV
36	868.5	21.8	508	4	AAB82317	Aab82317 Human imm
37	868.5	21.8	508	7	ADM35239	Adm35239 Human LY1
38	868.5	21.8	508	7	ADM35264	Adm35264 Human LY1
39	868.5	21.8	508	8	ADF89715	Adf89715 Human can
40	868.5	21.8	508	8	ADL06539	Adl06539 Human tum
41	864.5	21.7	445	7	ADM35268	Adm35268 Human LY1
42	864.5	21.7	489	7	ADF74316	Adf74316 Human FCR
43	858.5	21.5	380	7	ADF74334	Adf74334 Extracell
44	851.5	21.3	421	6	ABU99158	Abu99158 Novel hum
45	851.5	21.3	421	8	ADM93881	Adm93881 Human NOV

ALIGNMENTS

RESULT 1

AAB82313

ID AAB82313 standard; protein; 759 AA.

XX AAB82313;

XX 23-JUL-2001 (first entry)

XX Human immunoglobulin receptor isoform IRTA2a.

XX Immunoglobulin superfamily receptor translocation associated; IRTA;

KW IRTA2a; human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma;

KW myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..15

FT Protein 16..759

FT Modified-site 132..134

FT Modified-site 383..385

FT Modified-site 621..623

FT Modified-site 631..633

FT Modified-site 714..716

FT Modified-site 714..716

FT Modified-site 714..716

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New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor

Translocation Associated proteins, used to treat B cell malignancies including lymphomas and multiple myeloma.

Claim 3; Fig 18B-1-18B-2; 72pp; English.

The present sequence is that of the novel human immunoglobulin receptor, immunoglobulin superfamily receptor translocation associated protein isoform 2a (IRTA2a), an Ig receptor involved in the pathogenesis of lymphoma and melanoma. Efforts to identify genes involved in chromosomal aberrations affecting band 1q21 in multiple myeloma and B cell lymphoma led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding members of a novel subfamily of related receptors within the immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82314 and AAB82315). IRTA2a is a 759 amino acid secreted glycoprotein with 8 Ig-type domains followed by a unique C-terminus. IRTA2b diverges from IRTA2a at residue 560, extending for a further 32 residues. IRTA2c diverges from IRTA2a at residue 746 and extends for a further 231 residues. The IRTA genes display a specific pattern of expression in mature B cells. IRTA2 is expressed in GC centrocytes and in perifollicular cells, which may include immunoblasts and memory cells. The invention provides IRTA nucleic acids and proteins, and antibodies directed to an epitope of an IRTA protein. Methods are claimed for: detecting a B cell malignancy comprising a 1q21 chromosomal rearrangement using a nucleic acid molecule that specifically hybridises with a unique sequence of human IRTA1-5; and treating a subject having a B cell cancer by administering an anti-IRTA antibody or an antisense oligonucleotide that specifically hybridises to IRTA mRNA so as to prevent overexpression of IRTA protein and hence to arrest cell growth or induce cell death of cancer cells expressing IRTA. The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma, multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse large cell lymphoma and follicular lymphoma. The B cell lymphoma is selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-Hodgkin's lymphoma

Sequence 759 AA;

Query Match 100.0%; Score 3993; DB 4; Length 759;
Best Local Similarity 100.0%; Pred. No. 6.5e-248;
Matches 759; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPQKTKWYHR 60
Db 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPQKTKWYHR 60
QY 61 YLGEKILRETDPNILEVOESGEYRCQAGSPVHLDFSSASLILQAPLSVPEGDSVV 120
Db 61 YLGEKILRETDPNILEVOESGEYRCQAGSPVHLDFSSASLILQAPLSVPEGDSVV 120
QY 121 LRCRAKAEVTLNTIYKNDNVLAFLNKETDPIHACLKONGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNTIYKNDNVLAFLNKETDPIHACLKONGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVEPFTTRVLRASSFQPIGPNVTLTCTQLSLERSDVPLRFRFFRDDQTLGLGWS 240
Db 181 VKIQVEPFTTRVLRASSFQPIGPNVTLTCTQLSLERSDVPLRFRFFRDDQTLGLGWS 240
QY 241 LSPNFQITAMWKSQSGFWCKAATWPHSVISDSRSMLOVOIPASHVPLTLPSPKALNFE 300
Db 241 LSPNFQITAMWKSQSGFWCKAATWPHSVISDSRSMLOVOIPASHVPLTLPSPKALNFE 300
QY 301 GYKVTLHCETQDSLTLYRFRYHEGVPLRHKSVCRCERGASISFSLTTSNGNYCTADNG 360
Db 301 GYKVTLHCETQDSLTLYRFRYHEGVPLRHKSVCRCERGASISFSLTTSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHVPLNLSSPDLIPEGAKVTLHCEAQRGSPILYQFHEDAA 420
Db 361 LGAKPSKAVSLSVTPVSHVPLNLSSPDLIPEGAKVTLHCEAQRGSPILYQFHEDAA 420
QY 421 LERRANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLGITVPSHPVLTLSA 480
Db 421 LERRANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLGITVPSHPVLTLSA 480

QY 481 EALTREGATVTLHCEVQSGSPQILYQFVHEDMPLWSSSTPVGSRVFSFSLTEGHSNGNY 540
Db 481 EALTREGATVTLHCEVQSGSPQILYQFVHEDMPLWSSSTPVGSRVFSFSLTEGHSNGNY 540
QY 541 CTADNGFGPQRSEVSVLSFVTVPVSRPILTLRVPRAQAVVDLLELHCEAPRGSPILYWF 600
Db 541 CTADNGFGPQRSEVSVLSFVTVPVSRPILTLRVPRAQAVVDLLELHCEAPRGSPILYWF 600
QY 601 YHEDVTLGSSAPSGGSEAFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660
Db 601 YHEDVTLGSSAPSGGSEAFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660
QY 661 LTRAPRAQAVVDLLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720
Db 661 LTRAPRAQAVVDLLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720
QY 721 HSGIYSCADNGLAEQRSEMVTILKVAGEWALPTSSTSEN 759
Db 721 HSGIYSCADNGLAEQRSEMVTILKVAGEWALPTSSTSEN 759
RESULT 2
ADM35235
ID ADM35235 standard; protein; 759 AA.
XX ADM35235;
XX AC ADM35235;
XX 03-JUN-2004 (first entry)
XX Human LY448P cancer related protein for cancer detection method.
XX cytostatic; T-cell vaccine; detection; cancer;
XX chronic lymphocytic leukemia.
XX Homo sapiens.
XX WO2003077836-A2.
XX 25-SEP-2003.
XX 06-NOV-2002; 2002WO-US035728.
XX 06-NOV-2001; 2001US-00040862.
XX 23-MAY-2002; 2002US-00154884.
XX (CORI-) CORIXA CORP.
XX Gaiger A, Algate PA, Mannion J, Retter M;
XX WPI; 2003-756941/71.
XX Detecting cancer in a patient comprises contacting a biological sample from the patient with a binding agent that binds to a cancer-associated polypeptide and comparing the amount of polypeptide to a predetermined cutoff value.
XX Disclosure; SEQ ID NO 10460; 419pp; English.
XX The invention relates to a method of detecting (M1) cancer in a patient by: (i) contacting a biological sample from the patient with an agent that binds to any of three polypeptides given in the specification; (ii) detecting in a sample an amount of the peptide that binds to the binding agent; and (iii) comparing the amount of polypeptide present in the patient's sample to a predetermined cutoff value. The specification also discloses a separate method for detecting (M2) cancer in a patient by a method similar to M1, except that the detection agent is an oligonucleotide that binds to any of three polynucleotides given in the specification. M1 and M2 are useful for detecting the presence of cancer in a patient, especially chronic lymphocytic leukemia. The applicant has identified specific human polypeptides overexpressed in one or more types of hematological malignancies. This sequence corresponds to a protein used in the method of the invention.

SQ	Sequence 759 AA;	OS	Homo sapiens.
Query Match	100.0%; Score 3993; DB 7; Length 759;	XX	Key
Best Local Similarity	100.0%; Pred. No. 6.5e-248;	XX	Peptide
Matches 759; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		XX	Protein
QY 1	MLLWVILLVLPVSGQFARTPRIIIFLOPPWTVTFQGERVTLCKGFRFSPQTKWYHR 60	FT	/label= Signal_peptide
DB 1	MLLWVILLVLPVSGQFARTPRIIIFLOPPWTVTFQGERVTLCKGFRFSPQTKWYHR 60	FT	/label= Mature_protein
QY 61	YLKKEILRETPDNLIVQESGEYRCQAQSGPLSPVHLDFFSSASLILQAPLSVFGDSVV 120	FT	/note= "Asn is N-glycosylated"
DB 61	YLKKEILRETPDNLIVQESGEYRCQAQSGPLSPVHLDFFSSASLILQAPLSVFGDSVV 120	FT	/note= "Asn is N-glycosylated"
QY 121	LRCKRAEVTLNNTIYKNDNVLAFLNKRTPHIIHACLDKNGAYRCTGYKESCCPVSSNT 180	FT	/note= "Asn is N-glycosylated"
DB 121	LRCKRAEVTLNNTIYKNDNVLAFLNKRTPHIIHACLDKNGAYRCTGYKESCCPVSSNT 180	FT	/note= "Asn is N-glycosylated"
QY 181	VKIQVQEPFTRPVLRASSFQIPSGNPVTLTCETQLSLERSDVLRFRRDDQTGLGWS 240	FT	/note= "Asn is N-glycosylated"
DB 181	VKIQVQEPFTRPVLRASSFQIPSGNPVTLTCETQLSLERSDVLRFRRDDQTGLGWS 240	FT	/note= "Asn is N-glycosylated"
QY 241	LSPNFOITAMWSKDSGFYWCKAATMHSVSDSPRWIOVQIPASHPVLTLSPEKALNFE 300	FT	/note= "Asn is N-glycosylated"
DB 241	LSPNFOITAMWSKDSGFYWCKAATMHSVSDSPRWIOVQIPASHPVLTLSPEKALNFE 300	FT	/note= "Asn is N-glycosylated"
QY 301	GTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVCERGASISFSLTENSNGNYCTADNG 360	FT	/note= "transmembrane domain"
DB 301	GTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVCERGASISFSLTENSNGNYCTADNG 360	FT	/note= "putative consensus Src-homology 2 (SH2) binding domain"
QY 361	LGAKPSKAVSLSVTVPSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420	FT	/note= "putative consensus Src-homology 2 (SH2) binding domain"
DB 361	LGAKPSKAVSLSVTVPSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420	FT	/note= "putative consensus Src-homology 2 (SH2) binding domain"
QY 421	LERRSANSAGGVAISFSLTAHSGNYCTADNGFGQPSKAVSLITVPVSHPVLTLSA 480	XX	WO200138490-A2.
DB 421	LERRSANSAGGVAISFSLTAHSGNYCTADNGFGQPSKAVSLITVPVSHPVLTLSA 480	XX	31-MAY-2001.
QY 481	EALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGY 540	XX	28-NOV-2000; 2000WO-US032403.
DB 481	EALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGY 540	XX	29-NOV-1999; 99US-0168151P.
QY 541	CTADNGFGQPSKAVSLSVTVPSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 600	XX	(UYCO) UNIV COLUMBIA NEW YORK.
DB 541	CTADNGFGQPSKAVSLSVTVPSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 600	XX	Dalla-Favera R;
QY 601	YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCAANNGLVAQHSOTISLTVIPVSRPI 660	XX	WPI; 2001-355921/37.
DB 601	YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCAANNGLVAQHSOTISLTVIPVSRPI 660	XX	N-PSDB; AAF30952.
QY 661	LTFRAPRAQAVVGDLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720	XX	New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor Translocation Associated proteins, used to treat B cell malignancies including lymphomas and multiple myeloma.
DB 661	LTFRAPRAQAVVGDLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720	XX	Claim 3; Fig 18B-1-18B-2; 72pp; English.
QY 721	HSGIYCEADNGLEAQRSEWTLKVAGEWALPTSSTSEN 759	XX	The present sequence is that of the novel human immunoglobulin receptor, immunoglobulin superfamily receptor translocation associated protein isoform 2c (IRTA2c), an Fc receptor involved in the pathogenesis of lymphoma and melanoma. Efforts to identify genes involved in chromosomal aberrations affecting band Iq21 in multiple myeloma and B cell lymphoma led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding members of a novel subfamily of related receptors within the immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82313 and AAB82314). IRTA2c is the longest isoform. It is a type I transmembrane glycoprotein. Each SH2 binding site agrees with the immune receptor tyrosine-based inhibition motif (ITIM) consensus and is encoded by a separate exon. The IRTA genes display a specific pattern of expression in mature B cells. IRTA2 is expressed in GC centrocytes and in perifollicular cells, which may include immunoblasts and memory cells. The invention provides IRTA
DB 721	HSGIYCEADNGLEAQRSEWTLKVAGEWALPTSSTSEN 759	XX	
RESULT 3		XX	
AAB82315		XX	
ID	AAB82315 standard; protein; 977 AA.	XX	
XX		XX	
AC	AAB82315;	XX	
XX		XX	
DT	23-JUL-2001 (first entry)	XX	
XX	Human immunoglobulin receptor isoform IRTA2c.	XX	
DE	Immunoglobulin superfamily receptor translocation associated; IRTA;	XX	
KW	IRTA2c; human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma;	XX	
KW	myeloma; B cell malignancy; cancer; chromosome Iq21; diagnosis; therapy.	XX	

CC nucleic acids and proteins, and antibodies directed to epitopes of IRTA
CC proteins. Methods are claimed for: detecting a B cell malignancy
CC comprising a 1q21 chromosomal rearrangement using a nucleic acid molecule
CC that specifically hybridizes with a unique sequence of human IRTA1-5; and
CC treating a subject having a B cell cancer by administering an anti-IRTA
CC antibody or an antisense oligonucleotide that specifically hybridizes to
CC IRTA mRNA so as to prevent overexpression of IRTA protein and hence to
CC arrest cell growth or induce cell death of cancer cells expressing IRTA.
CC The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma,
CC Multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse
CC large cell lymphoma and follicular lymphoma. The B cell lymphoma is
CC selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-
CC Hodgkin's lymphoma
XX
XX
SQ Sequence 977 AA;

Query Match 98.2%; Score 3923; DB 4; Length 977;
Best Local Similarity 100.0%; Pred. No. 2.8e-243;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLWILLVLPVSGQFARTPRPIIFLOPPWTTVFGSERVLTCKGFRFYSFQTKWYHR 60
DB 1 MLLWILLVLPVSGQFARTPRPIIFLOPPWTTVFGSERVLTCKGFRFYSFQTKWYHR 60
QY 61 YLKGKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFFSSASLILOAPLSVFEQDSV 120
DB 61 YLKGKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFFSSASLILOAPLSVFEQDSV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFNKRTRDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFNKRTRDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLTCTQLSLERSDVLPRFRFRDQTLGLGWS 240
DB 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLTCTQLSLERSDVLPRFRFRDQTLGLGWS 240
QY 241 LSPNFQITAMWSKDSGYKCAATMHSVSDSPRWIQVOIPASHPVLTLSPKALNPE 300
DB 241 LSPNFQITAMWSKDSGYKCAATMHSVSDSPRWIQVOIPASHPVLTLSPKALNPE 300
QY 301 GTKVTLCHETQEDSLRTLYRFXHGVPLRHKSVCRCERGASISFSLTENSNGNYCTADNG 360
DB 301 GTKVTLCHETQEDSLRTLYRFXHGVPLRHKSVCRCERGASISFSLTENSNGNYCTADNG 360
QY 361 LGAKPSKAVLSVTVPSHPVNLNLSPEDLIFEGAKVTLHCEAQRGSLPILYOFHEDAA 420
DB 361 LGAKPSKAVLSVTVPSHPVNLNLSPEDLIFEGAKVTLHCEAQRGSLPILYOFHEDAA 420
QY 421 LERRANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVLSIITVPVSHPVLTLSA 480
DB 421 LERRANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVLSIITVPVSHPVLTLSA 480
QY 481 EALTPEGATVTLHCEVQSGPQILYQFVHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
DB 481 EALTPEGATVTLHCEVQSGPQILYQFVHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
QY 541 CTADNGFGPQRSVSLFVTVPSHPVNLNLSPEDLIFEGAKVTLHCEAQRGSPILYWF 600
DB 541 CTADNGFGPQRSVSLFVTVPSHPVNLNLSPEDLIFEGAKVTLHCEAQRGSPILYWF 600
QY 601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYYCANNGLVAQHSDDTISLVIIVPSRPI 660
DB 601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYYCANNGLVAQHSDDTISLVIIVPSRPI 660
QY 661 LTFRAPRAQAVVGDLELHCEALRGSSPLLYWFYHEDVTLGKISAPSGGASFNLSLTTE 720
DB 661 LTFRAPRAQAVVGDLELHCEALRGSSPLLYWFYHEDVTLGKISAPSGGASFNLSLTTE 720
QY 721 HSGIYSCDADNGLEAQRSEMWTLKVA 746
DB 721 HSGIYSCDADNGLEAQRSEMWTLKVA 746

RESULT 4

ADM35237
ADM35237 standard; protein; 977 AA.

XX
AC ADM35237;

XX
DT 03-JUN-2004 (first entry)

XX
Human LY1448P cancer related protein for cancer detection method.

XX
cytostatic; T-cell vaccine; detection; cancer;
chronic lymphocytic leukemia.

XX
Homo sapiens.

XX
WC2003077836-A2.

XX
25-SEP-2003.

XX
06-NOV-2002; 2002WO-US035728.

XX
06-NOV-2001; 2001US-00040862.

XX
23-MAY-2002; 2002US-00154884.

XX
(CORI-) CORIXA CORP.

XX
Gaiger A, Algate PA, Mannion J, Retter M;

XX
WPI; 2003-756941/71.

XX
Detecting cancer in a patient comprises contacting a biological sample
from the patient with a binding agent that binds to a cancer-associated
polypeptide and comparing the amount of polypeptide to a predetermined
cutoff value.

XX
Disclosure; SEQ ID NO 10462; 419pp; English.

XX
The invention relates to a method of detecting (M1) cancer in a patient
by: (i) contacting a biological sample from the patient with an agent
that binds to any of three polypeptides given in the specification; (ii)
detecting in a sample an amount of the peptide that binds to the binding
agent; and (iii) comparing the amount of polypeptide present in the
patient's sample to a predetermined cutoff value. The specification also
discloses a separate method for detecting (M2) cancer in a patient by a
method similar to M1, except that the detection agent is an
oligonucleotide that binds to any of three polynucleotides given in the
specification. M1 and M2 are useful for detecting the presence of cancer
in a patient, especially chronic lymphocytic leukemia. The applicants
have identified specific human polypeptides overexpressed in one or more
types of hematological malignancies. This sequence corresponds to a
protein used in the method of the invention.

XX
SQ Sequence 977 AA;

Query Match 98.2%; Score 3923; DB 7; Length 977;

Best Local Similarity 100.0%; Pred. No. 2.8e-243;

Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWILLVLPVSGQFARTPRPIIFLOPPWTTVFGSERVLTCKGFRFYSFQTKWYHR 60
DB 1 MLLWILLVLPVSGQFARTPRPIIFLOPPWTTVFGSERVLTCKGFRFYSFQTKWYHR 60
QY 61 YLKGKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFFSSASLILOAPLSVFEQDSV 120
DB 61 YLKGKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFFSSASLILOAPLSVFEQDSV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFNKRTRDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFNKRTRDFHIFACLDKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLTCTQLSLERSDVLPRFRFRDQTLGLGWS 240
DB 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLTCTQLSLERSDVLPRFRFRDQTLGLGWS 240


```
Qy 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIOVQIPASHPVLTLSPEKALNFE 300
Dy 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIOVQIPASHPVLTLSPEKALNFE 300
Qy 301 GTKVTLCETQEDSLRTLRYFHEGVPLRHKSVCERGASISFSLTTENSNGNYCTADNG 360
Dy 301 GTKVTLCETQEDSLRTLRYFHEGVPLRHKSVCERGASISFSLTTENSNGNYCTADNG 360
Qy 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA 420
Dy 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA 420
Qy 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
Dy 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
Qy 481 EALTPEGATVTLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGY 540
Dy 481 EALTPEGATVTLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGY 540
Qy 541 CTADNGFGPQRSSEVSLFVTPVSRPILTLRVPRQAQVVGDLLEHCEAPRGSPPILYWF 600
Dy 541 CTADNGFGPQRSSEVSLFVTPVSRPILTLRVPRQAQVVGDLLEHCEAPRGSPPILYWF 600
Qy 601 YHEDVTILGSSSAPSGGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660
Dy 601 YHEDVTILGSSSAPSGGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660
Qy 661 LTRAPRAQAVVGDLLEHCEALRGSSPILYWFYHEDVTILGKISAPSGGASFNLSLTTTE 720
Dy 661 LTRAPRAQAVVGDLLEHCEALRGSSPILYWFYHEDVTILGKISAPSGGASFNLSLTTTE 720
Qy 721 HSGIYSCADNGLEAQRSEMWTLKVA 746
Dy 721 HSGIYSCADNGLEAQRSEMWTLKVA 746

RESULT 5
ABP97215
ID ABP97215 standard; protein; 977 AA.
XX
AC ABP97215;
XX
01-JUL-2003 (first entry)
XX
Tumour-associated antigenic target protein TAT374 SEQ ID NO:97.
XX
Human; tumour-associated antigenic target; TAT; tumour; diagnosis;
XX
Homo sapiens.
XX
W0203024392-A2.
XX
27-MAR-2003.
XX
11-SEP-2002; 2002WO-US028859.
XX
18-SEP-2001; 2001US-0323268P.
XX
19-OCT-2001; 2001US-0339227P.
XX
07-NOV-2001; 2001US-0336827P.
XX
20-NOV-2001; 2001US-0331906P.
XX
03-JAN-2002; 2002US-0345444P.
XX
02-APR-2002; 2002US-0369724P.
XX
19-AUG-2002; 2002US-0404809P.
XX
(GETH ) GENENTECH INC.
XX
Frantz G. Hillan KJ, Phillips HS, Polakis P, Spencer SD;
PI Williams PM, Wu TD, Zhang Z;
XX
WPI; 2003-354551/33.
DR
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DR N-PSDB; ACC49533.
XX
PT New antibodies against tumor-associated antigenic target polypeptide,
PT useful for treating or diagnosing tumors or cancers in mammals, e.g.
PT prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
PT carcinomas.
XX
PS Claim 2; Fig 97; 285pp; English.
XX
CC ACC49493 to ACC49552 encode the human tumour-associated antigenic target
CC (TAT) proteins given in ABP97175 to ABP97234. The present invention
CC describes an isolated antibody that binds to a polypeptide having at
CC least 80 % sequence identity to any of the 60 150-800 residue amino acid
CC sequences (S1), given in ABP97175 to ABP97234, comprising (S1), lacking
CC its associated signal peptide, encoded by any of the 60 2000-3000 base
CC pair sequences (S2), given in ACC49493 to ACC49552. TAT proteins have
CC cytostatic activity. The antibody can be used for treating or diagnosing
CC tumours or cancers in mammals, e.g. prostate cancer, lung cancer, breast
CC cancer, colon cancer, ovarian cancer, prostate adenocarcinomas, renal
CC cell carcinomas, or thyroid cancer
XX
SQ Sequence 977 AA;
XX
Query Match 98.1%; Score 3916; DB 6; Length 977;
Best Local Similarity 99.9%; Pred. No. 8e-243;
Matches 745; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MLWLWILLVLAPVSGOPARTPRPIIFLOPPWTVFQGERVTLCKGRFYPSPQTKWYHR 60
Dy 1 MLWLWILLVLAPVSGOPARTPRPIIFLOPPWTVFQGERVTLCKGRFYPSPQTKWYHR 60
Qy 61 YLGEKILRETPDNILEVOESGEYRCQAQSGPLSPVHLDFSSASLILOAPLSVEGDSVV 120
Dy 61 YLGEKILRETPDNILEVOESGEYRCQAQSGPLSPVHLDFSSASLILOAPLSVEGDSVV 120
Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTFPHACLKONGAYRCTGYKESCCPVSSNT 180
Dy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTFPHACLKONGAYRCTGYKESCCPVSSNT 180
Qy 181 VKIQVQEPFTRPVLRASSFOPISGNPVTLTCTQLSLERSDVPRLRFFRDDOTLGLGWS 240
Dy 181 VKIQVQEPFTRPVLRASSFOPISGNPVTLTCTQLSLERSDVPRLRFFRDDOTLGLGWS 240
Qy 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIOVQIPASHPVLTLSPEKALNFE 300
Dy 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIOVQIPASHPVLTLSPEKALNFE 300
Qy 301 GTKVTLCETQEDSLRTLRYFHEGVPLRHKSVCERGASISFSLTTENSNGNYCTADNG 360
Dy 301 GTKVTLCETQEDSLRTLRYFHEGVPLRHKSVCERGASISFSLTTENSNGNYCTADNG 360
Qy 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA 420
Dy 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA 420
Qy 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
Dy 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
Qy 481 EALTPEGATVTLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGY 540
Dy 481 EALTPEGATVTLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGY 540
Qy 541 CTADNGFGPQRSSEVSLFVTPVSRPILTLRVPRQAQVVGDLLEHCEAPRGSPPILYWF 600
Dy 541 CTADNGFGPQRSSEVSLFVTPVSRPILTLRVPRQAQVVGDLLEHCEAPRGSPPILYWF 600
Qy 601 YHEDVTILGSSSAPSGGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660
Dy 601 YHEDVTILGSSSAPSGGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660
Qy 661 LTRAPRAQAVVGDLLEHCEALRGSSPILYWFYHEDVTILGKISAPSGGASFNLSLTTTE 720
Dy 661 LTRAPRAQAVVGDLLEHCEALRGSSPILYWFYHEDVTILGKISAPSGGASFNLSLTTTE 720
```

661 LTFRAPRAQAVVGDLELHCEALRGSSPILYFVHEDVTLGKISAPSGGASFNLSLTT 720

721 HSGIYSCADNGLAQRSEMTLVKA 746

721 HSGIYSCADNGLAQRSEMTLVKA 746

RESULT 6

ABM82476
ID ABM82476 standard; protein; 875 AA.

AC ABM82476;

DT 18-NOV-2004 (first entry)

XX Human diagnostic and therapeutic pprotein SEQ ID NO:2725.

DE gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX Homo sapiens.

OS WO2004023973-A2.

PN 25-MAR-2004.

XX 12-SEP-2003; 2003WO-US028227.

XX 12-SEP-2002; 2002US-0410259P.

PR 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
XX Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
XX Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
XX Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
XX Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
XX Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
XX Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
XX Patury S, Shi X, Suarez CJ;
XX WPI; 2004-329368/30.
DR N-PSDB; ACN41128.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
XX in diagnosing a condition, disease or disorder associated with human
XX molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
XX in gene mapping.

XX Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides
XX selected from one of the 722 sequences defined in the specification. A
XX polynucleotide of the invention may have a use in gene therapy. The human
XX polynucleotide and therapeutic polynucleotides (dithp) or polypeptides may be
XX used to diagnose a particular condition, disease or disorder associated
XX with human molecules, e.g. cell proliferative disorders,
XX autoimmune/inflammatory disorder, developmental disorder, endocrine
XX disorder, neurological disorders, gastrointestinal disorders, or
XX infections caused by virus, bacteria, fungi or parasite. The dithp
XX molecules may also be used in genetic mapping, in identifying individuals
XX from minute biological samples, in detecting single nucleotide
XX polymorphisms, as molecular weight markers, and for somatic or germline
XX gene therapy. The present sequence represents a dithp protein of the
XX invention. Note: The sequence data for this patent is not represented in
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX Sequence 875 AA;

Query Match 93.2%; Score 3720; DB 8; Length 875;
Best Local Similarity 95.6%; Pred. No. 2.7e-230;
Matches 715; Conservative 7; Mismatches 14; Indels 12; Gaps 3;

QY 1 MLLWVILLVLA PVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRYSPOKTKWYHR 60
DB 1 MLLWVILLVLA PVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRYSPOKTKWYHR 60
QY 61 YLGEKILRETDPNILEVQESGEYRCAQGSPLSSPVHLDPSSASLILQAPLSVFEQDSV 120
DB 61 YLGEKILRETDPNILEVQESGEYRCAQGSPLSSPVHLDPSSASLILQAPLSVFEQDSV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHACHLXNDGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHACHLXNDGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSFQPIISGNPVTLTCTQLSLERSDVLPRFRFRDDQTLGLWS 240
DB 181 VKIQVQEPFTRPVLRASSFQPIISGNPVTLTCTQLSLERSDVLPRFRFRDDQTLGLWS 240
QY 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVTSDSRWSIQVQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYWCKAATMPYSVTSDSRWSIQVQIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTLHCETQEDSLRTLRYRHYEGVPLRHKSVCRCGASISFSLTTENSNGNYCTADNG 360
DB 301 GTKVTLHCETQEDSLRTLRYRHYEGVPLRHKSVCRCGASISFSLTTENSNGNYCTADNG 360
QY 361 LGAXPSKAVLSVTVPVSHPVNLSSPEDLI FEGAKVTLHCEAQRGSLPILYOFHHEDAA 420
DB 361 LGAXPSKAVLSVTVPVSHPVNLSSPEDLI FEGAKVTLHCEAQRGSLPILYOFHHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVLSITVPVSHPVLTLSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVLSITVPVSHPVLTLSA 480
QY 481 EALTFEAGATVTLHCEVORGSPQILYQFVHEDMPLWSSSTPSVGRVSFSLTECHSGNYY 540
DB 481 EALTFEAGATVTLHCEVORGSPQILYQFVHEDMPLWSSSTPSVGRVSFSLTECHSGNYY 540
QY 541 CTADNGFGPQRSSEVVSFLF-VTVPVSRPILTLRVPRAAVVDLLELHCEAPRGSPPIIYW 599
DB 541 CTADNGFGPQRSSEVVSFLF-VTVPVSRPILTLRVPRAAVVDLLELHCEAPRGSPPIIYW 599
QY 600 FYHEDVTLGSSAPSGGEASFNLSITAEHSGNYSCEANGLVAQHSDTISLSVTPVSRP 659
DB 601 FYHEDVTLGSSAPSGGEASFNLSITAEHSGNYSCEANGLVAQHSDTISLSVTPVSRP 660
QY 660 ILTFRAPRAQAVVGDLELHCEALRGSSPILYFVHEDVTLGKISAPSGGASFNLSLTT 719
DB 661 ILTFR-----LLELHCEALRGSSPILYFVHEDVTLGKISAPSGGASFNLSLTTA 709
QY 720 EHSIGYSCADNGLAQRSEMTLVKA 747
DB 710 EHSIGYSCADNGLAQRSEMTLVKA 737

RESULT 7

ABM82477

ID ABM82477 standard; protein; 837 AA.

XX ABM82477;

XX 18-NOV-2004 (first entry)

DT Human diagnostic and therapeutic pprotein SEQ ID NO:2726.

DE gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX Homo sapiens.

OS WO2004023973-A2.

PN 25-MAR-2004.

XX 12-SEP-2003; 2003WO-US028227.

XX 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX (INCY-) INCYTE CORP.
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EN, Deleane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gersin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kitron ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patruy S, Shi X, Suarez CJ;
XX WPI; 2004-329368/30.
DR N-PSDB; ACN41129.
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX Claim 27; Page; 190pp; English.
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorders, developmental disorders, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX Sequence 837 AA;
SQ Query Match 87.3%; Score 3487; DB 8; Length 837;
Best Local Similarity 90.4%; Pred. No. 2.4e-215;
Matches 676; Conservative 7; Mismatches 15; Indels 50; Gaps 4;
QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVQGERVTLCKGFRFYSPOKTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVQGERVTLCKGFRFYSPOKTKWYHR 60
QY 61 YLGEILRETPDNLLEVOESGEYRCQAQSGPLSPVHLDPESSASLILQAPLSFEGDSVY 120
DB 61 YLGEILRETPDNLLEVOESGEYRCQAQSGPLSPVHLDPESSASLILQAPLSFEGDSVY 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTFPHACLKNDGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTFPHACLKNDGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVEPFRPVLRASSFOPIISGNPVTLCETQLSLERSDVLPRFRFRDDQTLGLGWS 240
DB 181 VKIQVEPFRPVLRASSFOPIISGNPVTLCETQLSLERSDVLPRFRFRDDQTLGLGWS 240
QY 241 LSPNFOITAMWSKDSGYWCKAATMPSVSDSPRSWIQVOIPASHPVLTLSEKALNFE 300
DB 241 LSPNFOITAMWSKDSGYWCKAATMPSVSDSPRSWIQVOIPASHPVLTLSEKALNFE 300
QY 301 GKTVTLHCETQEDSLRTLRYFHEGVPLRHKSVCRCERGASISFSLTTENSNGNYCTADNG 360
DB 282 -----XFYHEGVPLRHKSVCRCERGASISFSLTTENSNGNYCTADNG 322
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420

DB 323 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 382
QY 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSVTPVSHPVLTLSA 480
DB 383 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSVTPVSHPVLTLSA 442
QY 481 EALTPEGATVTLHCEVQSGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSGNY 540
DB 443 EALTPEGATVTLHCEVQSGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSGNY 502
QY 541 CTADNGFGPORSVSLF-VTVVPSRPILTLRPRAQAVVDLLELHCEAPRSPPIYLW 599
DB 503 CTADNGFGPORSVSLF-VTVVPSRPILTLRPRAQAVVDLLELHCEAPRSPPIYLW 562
QY 600 FYHEDVTLGSSSAPSGEASFNLSLTAHSGNYSCEANGLVAQHSOTISLSLTVPSR 659
DB 563 FYHEDVTLGSSSAPSGEASFNLSLTAHSGNYSCEANGLVAQHSOTISLSLTVPSR 622
QY 660 ILTFRAPRAQAVVDLLELHCEALRGSSPILYQFYHEDVTLGKISAPSGGASFNLSLT 719
DB 623 ILTFR-----LLELHCEALRGSPILYQFYHEDVTLGKISAPSGGASFNLSLT 671
QY 720 EHSGLYSCADNGLGAQRSEMTLVKAG 747
DB 672 EHSGLYSCADNGLGAQRSEMTLVKAG 699
RESULT 8
AAB82314
ID AAB82314 standard; protein; 592 AA.
XX AAB82314;
AC AAB82314;
DT 23-JUL-2001 (first entry)
XX Human immunoglobulin receptor isoform IRTA2b.
DE Immunoglobulin superfamily receptor translocation associated; IRTA2b.
XX IRTA2b; human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma;
KW myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.
XX Homo sapiens.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..15
FT Protein /label= Signal_peptide
FT Protein 16..592
FT Modified-site /label= Mature_protein
FT Modified-site 132..134
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site 383..385
FT Modified-site /note= "Asn is N-glycosylated"
PN W0200138490-A2.
XX 31-MAY-2001.
XX 28-NOV-2000; 2000WO-US032403.
XX 29-NOV-1999; 99US-0168151P.
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX Dalla-Favera R;
XX WPI; 2001-355921/37.
DR N-PSDB; AAF30951.
XX New genes encoding immunoglobulin receptor, immunoglobulin super Receptor
PT translocation Associated proteins, used to treat B cell malignancies
PT including lymphomas and multiple myeloma.
XX

Claim 3; Fig 18B-1-18B-2; 72pp; English.

PS The present sequence is that of the novel human immunoglobulin receptor,
XX immunoglobulin superfamily receptor translocation associated protein
CC isoform 2b (IRTA2b), an FC receptor involved in the pathogenesis of
CC lymphoma and melanoma. Efforts to identify genes involved in chromosomal
CC aberrations affecting band 1q21 in multiple myeloma and B cell lymphoma
CC led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding
CC members of a novel subfamily of related receptors within the
CC immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA
CC isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82314 and AAB82315).
CC IRTA2b is a 592 amino acid glycoprotein, which diverges from IRTA2a at
CC residue 560, extending for a further 32 residues, whose hydrophobicity
CC suggest docking to the plasma membrane via a GPI anchor. The IRTA2 genes
CC display a specific pattern of expression in mature B cells. IRTA2 is
CC expressed in GC centrocytes and in perifollicular cells, which may
CC include immunoblasts and memory cells. The invention provides IRTA
CC nucleic acids and proteins, and antibodies directed to an epitope of an
CC IRTA protein. Methods are claimed for: detecting a B cell malignancy
CC comprising a 1q21 chromosomal rearrangement using a nucleic acid molecule
CC that specifically hybridises with a unique sequence of human IRTA1-5; and
CC treating a subject having a B cell cancer by administering an anti-IRTA
CC antibody or an antisense oligonucleotide that specifically hybridises to
CC IRTA mRNA so as to prevent overexpression of IRTA protein and hence to
CC arrest cell growth or induce cell death of cancer cells expressing IRTA.
CC The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma,
CC multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse
CC large cell lymphoma and follicular lymphoma. The B cell lymphoma is
CC selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-
CC Hodgkin's lymphoma

XX Sequence 592 AA;

Query Match 74.2%; Score 2962; DB 4; Length 592;
Best Local Similarity 98.6%; Pred. No. 8.3e-182;
Matches 564; Conservative 0; Mismatches 4; Indels 4; Gaps 1;
QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPTWTFQGERVTLTKGFRFYSQKTKWYHR 60
DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPTWTFQGERVTLTKGFRFYSQKTKWYHR 60
QY 61 YLGEKILRETPDNLVEQESGEYRCQAQGSPLSSPVHLDFFSSASLILOAPLSVFEQDSVY 120
DB 61 YLGEKILRETPDNLVEQESGEYRCQAQGSPLSSPVHLDFFSSASLILOAPLSVFEQDSVY 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLDKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLDKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVEPFTPLVLRASSFPQISGNPVTLCETQLSLERSDVLPRFRFRDDQTLGLGWS 240
DB 181 VKIQVEPFTPLVLRASSFPQISGNPVTLCETQLSLERSDVLPRFRFRDDQTLGLGWS 240
QY 241 LSPNQITAMWSKDSGFYWCXKAATPHSVISDSFRSMIQVQIPASHPVLTLSPKALNFE 300
DB 241 LSPNQITAMWSKDSGFYWCXKAATPHSVISDSFRSMIQVQIPASHPVLTLSPKALNFE 300
QY 301 GPKVTLHCETQEDSLRTLYRFHEGVPLRHKSVCERGASISFSLTTENSNNYCTADNG 360
DB 301 GPKVTLHCETQEDSLRTLYRFHEGVPLRHKSVCERGASISFSLTTENSNNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA 420
DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNNYCTADNGFGPQRKAVSLISITPVSHPVLTLSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNNYCTADNGFGPQRKAVSLISITPVSHPVLTLSA 480
QY 481 EALTTEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPVSGRVVSFSLTEGHSGNY 540
DB 481 EALTTEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPVSGRVVSFSLTEGHSGNY 540

QY 541 CTADNGFGPQRSEVVSFLFVT-----VPVSRPIL 568
DB 541 CTADNGFGPQRSEVVSFLFVTGKCVLASHPPL 572

RESULT 9

ADM35236

ID ADM35236 standard; protein; 592 AA.

XX ADM35236;

XX 03-JUN-2004 (first entry)

XX Human LY1448P cancer related protein for cancer detection method.

XX cytostatic; T-cell vaccine; detection; cancer;

XX chronic lymphocytic leukemia.

XX Homo sapiens.

XX WO2003077836-A2.

XX 25-SEP-2003.

XX 06-NOV-2002; 2002WO-US035728.

XX 06-NOV-2001; 2001US-00040862.

XX 23-MAY-2002; 2002US-00154884.

XX (CORI-) CORIXA CORP.

XX Gaiger A, Algate PA, Mannion J, Retter M;

XX WPI; 2003-756941/71.

XX Detecting cancer in a patient comprises contacting a biological sample

XX from the patient with a binding agent that binds to a cancer-associated

XX polypeptide and comparing the amount of polypeptide to a predetermined

XX cutoff value.

XX Disclosure; SEQ ID NO 10461; 419pp; English.

XX The invention relates to a method of detecting (M1) cancer in a patient

XX by: (i) contacting a biological sample from the patient with an agent

XX that binds to any of three polypeptides given in the specification; (ii)

XX detecting in a sample an amount of the peptide that binds to the binding

XX agent; and (iii) comparing the amount of polypeptide present in the

XX patient's sample to a predetermined cutoff value. The specification also

XX discloses a separate method for detecting (M2) cancer in a patient by a

XX method similar to M1, except that the detection agent is an

XX oligonucleotide that binds to any of three polynucleotides given in the

XX specification. M1 and M2 are useful for detecting the presence of cancer

XX in a patient, especially chronic lymphocytic leukemia. The applicants

XX have identified specific human polypeptides overexpressed in one or more

XX types of hematological malignancies. This sequence corresponds to a

XX protein used in the method of the invention.

XX Sequence 592 AA;

Query Match 74.2%; Score 2962; DB 7; Length 592;

Best Local Similarity 98.6%; Pred. No. 8.3e-182;

Matches 564; Conservative 0; Mismatches 4; Indels 4; Gaps 1;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPTWTFQGERVTLTKGFRFYSQKTKWYHR 60

DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPTWTFQGERVTLTKGFRFYSQKTKWYHR 60

QY 61 YLGEKILRETPDNLVEQESGEYRCQAQGSPLSSPVHLDFFSSASLILOAPLSVFEQDSVY 120

DB 61 YLGEKILRETPDNLVEQESGEYRCQAQGSPLSSPVHLDFFSSASLILOAPLSVFEQDSVY 120

QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLDKNGAYRCTGYKESCCPVSSNT 180

DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLDKNGAYRCTGYKESCCPVSSNT 180

Db 121 LRCRAKEVTLNNTIYKNDNVLAFLNKRTPHPIHACLKONGAYRCTGYKESCCPVSSNT 180
Qy 181 VKIQVQEPFTRPVLASSFQISGNPVTLTCTETQLSLERSDVPPLRFRFRDDQTLGLGWS 240
Db 181 VKIQVQEPFTRPVLASSFQISGNPVTLTCTETQLSLERSDVPPLRFRFRDDQTLGLGWS 240
Qy 241 LSPNFQITAMWSKDSGYWCKAATMPHSVTSDSRSPWIOVQIPASHPVLTLSPEKALNFE 300
Db 241 LSPNFQITAMWSKDSGYWCKAATMPHSVTSDSRSPWIOVQIPASHPVLTLSPEKALNFE 300
Qy 301 GTKVTLTCEQDSRLTLYRFXHGVPLRHKSVCRCGASISFSLTTEGSGNYCTADNG 360
Db 301 GTKVTLTCEQDSRLTLYRFXHGVPLRHKSVCRCGASISFSLTTEGSGNYCTADNG 360
Qy 361 LGAKPSKAVSLSVTPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQFHHEDAA 420
Db 361 LGAKPSKAVSLSVTPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQFHHEDAA 420
Qy 421 LERRSANSAGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSA 480
Db 421 LERRSANSAGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSA 480
Qy 481 EALTFFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSPFSLTECHSGNY 540
Db 481 EALTFFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSPFSLTECHSGNY 540
Qy 541 CTADNGFGPQRSEVSVLFTVTPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQFHHEDAA 568
Db 541 CTADNGFGPQRSEVSVLFTVTPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQFHHEDAA 572
RESULT 10
ID ABU99155 standard; protein; 582 AA.
AC ABU99155;
XX
DT 01-AUG-2003 (first entry)
XX
DE Novel human GPCR related protein NOV17a.
XX
KW Human; G-protein coupled receptor related protein; GPCR related protein; NOV; cytosolic; cardiant; antiarteriosclerotic; antidiabetic;
KW immunomodulator; anti-HIV; anorectic; antiasthmatic; haemostatic;
KW antiparkinsonian; neuroprotective; nootropic; gene therapy; vaccine;
KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer;
KW diabetes; immune disorder; AIDS; obesity; asthma;
KW haematopoietic disorder; Parkinson's disease; Alzheimer's disease;
KW infection; multiple sclerosis; cancer-associated cachexia;
KW wasting disorder; chronic disease; neurogenesis; cell differentiation;
KW cell proliferation; haematopoiesis; wound healing; angiogenesis;
KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.
XX Homo sapiens.
OS
XX
PN WO200299116-A2.
XX
XX
PD 12-DEC-2002.
XX
PF 04-JUN-2001; 2002WO-US017428.
XX
PR 04-JUN-2001; 2001US-0295607P.
PR 04-JUN-2001; 2001US-0295661P.
PR 06-JUN-2001; 2001US-0296404P.
PR 06-JUN-2001; 2001US-0296418P.
PR 14-JUN-2001; 2001US-0298285P.
PR 15-JUN-2001; 2001US-0298556P.
PR 21-JUN-2001; 2001US-0299949P.
PR 26-JUN-2001; 2001US-0300883P.
PR 28-JUN-2001; 2001US-0301550P.
PR 13-AUG-2001; 2001US-0311972P.
PR 27-AUG-2001; 2001US-0315071P.
PR 29-AUG-2001; 2001US-0315660P.

PR 14-SEP-2001; 2001US-0322993P.
PR 17-SEP-2001; 2001US-0322706P.
PR 14-DEC-2001; 2001US-0341186P.
PR 28-FEB-2002; 2002US-0361189P.
PR 12-MAR-2002; 2002US-0363673P.
PR 12-MAR-2002; 2002US-0363676P.
PR 03-JUN-2002; 2002US-00363676.
XX (CURA-) CURAGEN CORP.
PA
XX
PI Anderson DW, Baumgartner JC, Boldog FL, Casman SJ, Edinger SR,
PI Gangolli EA, Gerlach VL, Gorman L, Guo X, Hjalt T, Kekuda R, Li L;
PI Macdougall JR, Malyankar UM, Millet I, Padigaru M, Patturajan M; CAM;
PI Pena CE, Rastelli L, Shimkets RA, Stone DJ, Spytek KA, Vernet BD;
PI Voss EZ, Zershusen BD;
XX WPI; 2003-140627/13.
DR N-PSDB; ACD03659.
XX
XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
PS Claim 1; Page 166; 332pp; English.
XX
CC The invention describes an isolated polypeptide (I) comprising any of 27
CC 118-961 residue amino acid sequences, given in the specification, a
CC mature form of them, a sequence that is at least 95 % identical to them,
CC or a sequence having one or more conservative substitutions in them. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease selected from a pathology
CC associated with the polypeptide. The NOVX polypeptides, polynucleotides
CC and antibodies are useful in treating or preventing NOVX-associated
CC disorders, e.g. cardiomyopathy, atherosclerosis, cancer, diabetes, immune
CC disorders, AIDS, obesity, asthma, haematopoietic disorders, Parkinson's
CC disease, Alzheimer's disease, infections, multiple sclerosis, cancer-
CC associated cachexia, and other wasting disorders associated with chronic
CC diseases. The nucleic acids and polypeptides may also be used as targets
CC for the identification of small molecules that modulate or inhibit e.g.
CC neurogenesis, cell differentiation, cell proliferation, haematopoiesis,
CC wound healing and angiogenesis, in gene therapy, in generation of
CC antibodies that bind immunospecifically to NOVX substances for use in
CC therapeutic or diagnostic methods. The nucleic acids are further used as
CC hybridisation probes, in chromosome mapping, tissue typing, preventive
CC medicine, and pharmacogenomics. The polypeptides are also useful as
CC vaccines. This is the amino acid sequence of a novel human G-protein
CC coupled receptor related protein NOV
XX
SQ Sequence 582 AA;
Query Match 35.5%; Score 1419.5; DB 6; Length 582;
Best Local Similarity 41.7%; Pred. No. 1e-82;
Matches 316; Conservative 72; Mismatches 175; Indels 195; Gaps 9;
Qy 1 MLLWVILLVLPVSGQFARTPRPIILQPEWTTVFGERVLTACKGRFYSPO-KTKWYH 59
Db 1 MLLWVILLVLPVSGQFARTPRPIILQPEWTTVFGERVLTACKGRFYSPO-KTKWYH 60
Qy 60 RYLGKILRETPDNILEVOESGYRCAQGSPLSSPVHLDFSSASLILQAPLSVFEGDSV 119
Db 61 ---DEKLLIKHKDKI-QITEPGNYQCKTRGSSLSDAVHVEFSPDWLILQALHPVFEQDNV 116
Qy 120 VLRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHPIHACLKONGAYRCTGYKESCC 176
Db 117 ILRCQKDNKNTKQKYYKDGKOLPNSYNLEKTVNSVRDMSKYNKCHCTATRKFYLDIEV 176
Qy 177 SSNTVQIQVEPFRPVLASSFQISGNPVTLTCTETQLSLERSDVPPLRFRFRDDQTLG 236
Db 177 TSKPLNIQVQELFHPVLRASSSTPIEGSPMTLTCTETQLSPQPDVQLQSLFRDSTL 236
Qy 237 LGWSLSPNFQITAMWSKDSGYWCKAATMPHSVTSDSRSPWIOVQIPASHPVLTLSPEKA 296
Db 237 LGWSLSPNFQITAMWSKDSGYWCKAATMPHSVTSDSRSPWIOVQIPASHPVLTLSPEKA 296

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Db 237 LWSRSPRLQIPAMWTDGSGYWCVEVTWTHSIKRSLSRQIRVQ----- 281
Qy 297 LNFEGTKVTLHCETQEDSLRTLRYFHEGVPLRHKSVRCERGASTSFLTTTNSGNYCT 356
Db 282 ----- 281
Qy 357 ADNGLGAKPSKAVSLVTVPVSHVPLNLSPPDLIFEGAKVTLHCEAQRGSLPILYQFHH 416
Db 282 -----RVPSNVNLEIRPTGGQLIEGENMVLICSVAGQSGTTFVSHK 324
Qy 417 ED--AALERSANSAGVAISFSLTAHSGNYCTADNGFGPORSKAVSLGITVPVSHPV 474
Db 325 EGRVSLGRKT-----QRLLAELH-----V 345
Qy 475 LTLSSAEALTFEAGTATLHCEVQSGPQILYQFYHEDMPLNSSSTPVSGRVFSFSLTEG 534
Db 346 LIVKESDA----- 353
Qy 535 HSGNYCTADNGFGPORSSEVSLFVTVPSRPILTLRVPRQAQVVDLLELHCEAPRGSP 594
Db 354 --GRYYCAADNVHSPILSTWIRVTRIPVSHVPLTFRAPRAHTVVGDLLELHCESLRGSP 411
Qy 595 PILYFVYHEDVTLGSSSAPSGEASPNLSLTAHSGNYSCEANNGIQAQHSPTISLSVIV 654
Db 412 PILYFVYHEDVTLGNSAASGASPNLSLTAHSGNYSCEADNGLGAQSHGVSLRVTV 471
Qy 655 PVSRLPILTFRAPRAQAVVGDLELHCEALRGSPILYFVYHEDVTLGKISAPSGGASFN 714
Db 472 PVSRLPILTRAPQAQAVVGDLELHCEALRGSPILYFVYHEDVTLGKISAPSGGASFN 531
Qy 715 LSLTTHSGIYSCAENGLEAQBSEMVTLKAVGEWALP 752
Db 532 LSLTTHSGIYSCAENGLEAQBSEMVTLKAVGEWALP 569
RESULT 11
ADN93875
ID ADM93875 standard; protein; 582 AA.
XX AC ADM93875;
DT 17-JUN-2004 (first entry)
XX DE Human NOV protein #47.
XX KW gene therapy; vaccine; NOVX; cancer; neurodegenerative disorder;
KW Parkinson's disease; metabolic disorder; diabetes; obesity;
KW immune related disorder; tissue typing; human.
XX OS Homo sapiens.
XX PN US2004009480-A1.
XX PD 15-JAN-2004.
XX PF 03-JUN-2002; 2002US-00162335.
XX PR 04-JUN-2001; 2001US-0295607P.
PR 04-JUN-2001; 2001US-0295661P.
PR 06-JUN-2001; 2001US-0296404P.
PR 06-JUN-2001; 2001US-0296418P.
PR 11-JUN-2001; 2001US-0297414P.
PR 12-JUN-2001; 2001US-0297567P.
PR 14-JUN-2001; 2001US-0298285P.
PR 15-JUN-2001; 2001US-0298556P.
PR 21-JUN-2001; 2001US-0299949P.
PR 26-JUN-2001; 2001US-0300883P.
PR 28-JUN-2001; 2001US-0301500P.
PR 13-AUG-2001; 2001US-0311972P.
PR 27-AUG-2001; 2001US-0315071P.
PR 29-AUG-2001; 2001US-0315660P.
PR 14-SEP-2001; 2001US-0322293P.

PR 17-SEP-2001; 2001US-0322706P.
PR 14-DEC-2001; 2001US-0341186P.
PR 28-FEB-2002; 2002US-0361189P.
PR 12-MAR-2002; 2002US-0363673P.
PR 12-MAR-2002; 2002US-0363676P.
XX
PA (ANDE/) ANDERSON D W.
PA (BAIM/) BAUMGARTNER J C.
PA (BOLD/) BOLDOG F L.
PA (CASM/) CASMAN S J.
PA (EDIN/) EDINGER S R.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUOX/) GUO X S.
PA (HUAL/) HJALT T.
PA (KEKU/) KEKUDA R.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATI/) PATTURAJAN M.
PA (PENA/) PENNA C E A.
PA (RAST/) RASTELLI L.
PA (SHIM/) SHIMKETS R A.
PA (STON/) STONE D J.
PA (SPYT/) SPYTEK K A.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.
XX
PI Anderson DW, Baumgartner JC, Boldog FL, Casman SJ, Edinger SR, Gangolli EA, Gerlach V, Gorman L, Guo XS, Hjalte T, Kekuda R, Li L; MacDougall JR, Malyankar UM, Millet I, Padigaru M, Patturajan M; Pena CE, Rastelli L, Shimkets RA, Stone DJ, Spytek KA, Vernet CM; Voss EZ, Zerhusen BD;
DR WPI: 2004-090456/09.
DR N-PSDB; ADM93874.
XX
PT New NOVX polypeptide, useful for preparing a composition for treating or preventing e.g., cancer, neurodegenerative disorders such as Parkinson's disease, or metabolic disorders such as diabetes or obesity, or for tissue typing.
PT
PT
PT
PS Claim 1; SEQ ID NO 94; 202pp; English.
XX
CC The invention relates to an isolated NOVX polypeptide. The polypeptide is useful for preparing a composition for treating or preventing a pathology associated with NOVX polypeptide e.g. cancer, neurodegenerative disorders such as Parkinson's disease, metabolic disorders such as diabetes or obesity or immune related disorders or for tissue typing. The present sequence represents a human NOV protein.
XX
SQ Sequence 582 AA;
Query Match 35.5%; Score 1419.5; DB 8; Length 582;
Best Local Similarity 41.7%; Pred. No. 1e-82;
Matches 316; Conservative 72; Mismatches 175; Indels 195; Gaps 9;
Qy 1 MLILWVLLVLAIPVSGQFARTPRPIIFLOPPVTVTFQGERVTLTKGFRFYSQ-KTKWYH 59
Db 1 MLILWVLLVLLTPGREGSGVAPKAVILLNPWTAFKGEKVALICSSISHLAAGDTYWH 60
Qy 60 RYLKGEILRETPDNILEVQESGEYRCQAQSGPLSSPVHLDFSSASLILQAPLSVFEQDSV 119
Db 61 ---DEKLLIKHDKI-QITEPGNYQCKTRGSSLSDAVHVEFSPDWLILQALHPVFEQDNV 116
Qy 120 VLFCRAKAEVTLNNTIYKNDNVLAFLNKRDTPHIACLKDKNGAYRCTGCKESC---CPV 176
Db 117 ILRCQCKDNKNTKQVYYKDGKQLPNSYNLEKITVNSVSRDNSKXHYCTAYRKFIYLDIEV 176

```
QY 177 SNTVKIQVQEPTRPVRASSPOISGNPVTLTCETQLSLERSDVLPRFRFRDDOTLG 236
Db 177 TSRLNIQVQELFLHPLVRASSSTPIEGSPMTLTCTQLSPQRPDVLQSLFRSDOTLG 236
QY 237 LGWSLSPNFQITAMWSKDSGYMCKAATMPHSVISDSRSPWIOVQIPASHVLTLSPEKA 296
Db 237 LGWSRSPRLQIPAMWTEDSSGYMCEVETVTHSIKRSLSQIRVQ----- 281
QY 297 LNFEGTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCRCGASISFSLTENSNGNYCT 356
Db 282 ----- 281
QY 357 ADNGLGAKPSKAVSLSVTPVSHPLNLSPEDLIFEGAKVTLHCEAQRGLPILYQFHH 416
Db 282 -----RVPSNVNLEIRPTGGQIEGENNVILCSVAQSGSTVTFSMWK 324
QY 417 ED--AALERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPORSKAVSLSVTPVSHPV 474
Db 325 EGRVRSIGRKT-----QRLLAELH-----V 345
QY 475 LTLSSAALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEG 534
Db 346 LTVKESDA----- 353
QY 535 HSGNYYCTADNGFGPORSSEVSVLFTVPVSRPILTLRVPRQAQVVGDLLELHCEAPRGSP 594
Db 354 --GRYYCAADNVHSPILSTWIRVTIRIPVSHPLTFRAPRAHTVVGDLLELHCESLRGSP 411
QY 595 PILYFYHEDVTLGSSAPSGGASFNLSLTAHSGNYSCEANGLVAQHSIDTISLSVIV 654
Db 412 PILYFYHEDVTLGNSAPSGGASFNLSLTAHSGNYSCEADNGLGAQHSIGVSLRVTV 471
QY 655 PVSRLPILTFRAPRAQAVVGDLLELHCEALRGSSPILYFYHEDVTLGKISAPSGGGASFN 714
Db 472 PVSRLPILTRAPGAQAVVGDLLELHCESLRGSPILYFYHEDVTLGNIHSAHSGGGASFN 531
QY 715 LSLTTEHSGIYSCAENGLRAQRSEMTLKVAGEWALP 752
Db 532 LSLTTEHSGNYSCEADNGLGAQHSKVTLNVTGLVLP 569

RESULT 12
ID ADM06089
XX ADM06089 standard; protein; 707 AA.
AC ADM06089;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human protein of the invention SEQ ID NO:4774.
XX
KW human; gene therapy; diagnostic marker; pharmaceutical.
XX
OS Homo sapiens.
XX
PN EP1347046-A1.
XX
PD 24-SEP-2003.
XX
PF 12-APR-2002; 2002EP-00008400.
XX
PR 22-MAR-2002; 2002JP-00137785.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-723558/69.
DR N-PSDB; ADM03646.
XX
PT New polynucleotides and polypeptides are useful in gene therapy, for
```

developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.

Claim 1; SEQ ID NO 4774; 305pp; English.

The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a protein sequence of the invention.

Sequence 707 AA;

Query Match 35.5%; Score 1417.5; DB 7; Length 707;
Best Local Similarity 41.6%; Pred. No. 1.8e-82;
Matches 318; Conservative 71; Mismatches 173; Indels 203; Gaps 10;

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QY 1 MLLWVILLVLPVSGOPARTPRPIIFLOPPMTTVFOGERVTLCKGRFFYSPO-KTKWYH 59
Db 1 MLLWVILLVLPVSGOPARTPRPIIFLOPPMTTVFOGERVTLCKGRFFYSPO-KTKWYH 60
QY 60 RYLKGBILRETPNILEVQESGEYRQAOQSPSSPVHLDFSSASLILQAPLSVFEGDSV 119
Db 61 ---DEKLLKIKHDKI-QITEPGNYCKTRGSSLSDAHVFEFSPDWLILQALHPVEGDNV 116
QY 120 VLRCAKAEVTLNNTYIKNDNVLAFLNKRDTFHI PHACLKNDGAYRCTGYKESC---CPV 176
Db 117 ILRCQCKNDKNTQKVVYKDGKQLPNSYNLEKIVTNSVSRDNSKYCHTAYRKFYLDIEV 176
QY 177 SNTVKIQVQEPTRPVRASSPOISGNPVTLTCETQLSLERSDVLPRFRFRDDOTLG 236
Db 177 TSRLNIQVQELFLHPLVRASSSTPIEGSPMTLTCTQLSPQRPDVLQSLFRSDOTLG 236
QY 237 LGWSLSPNFQITAMWSKDSGYMCKAATMPHSVISDSRSPWIOVQIPASHVLTLSPEKA 296
Db 237 LGWSRSPRLQIPAMWTEDSSGYMCEVETVTHSIKRSLSQIRVQ----- 281
QY 297 LNFEGTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCRCGASISFSLTENSNGNYCT 356
Db 282 ----- 281
QY 357 ADNGLGAKPSKAVSLSVTPVSHPLNLSPEDLIFEGAKVTLHCEAQRGLPILYQFHH 416
Db 282 -----RVPSNVNLEIRPTGGQIEGENNVILCSVAQSGSTVTFSMWK 324
QY 417 ED--AALERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPORSKAVSLSVTPVSHPV 474
Db 325 EGRVRSIGRKT-----QRLLAELH-----V 345
QY 475 LTLSSAALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEG 534
Db 346 LTVKESDA----- 353
QY 535 HSGNYYCTADNGFGPORSSEVSVLFTVPVSRPILTLRVPRQAQVVGDLLELHCEAPRGSP 594
Db 354 --GRYYCAADNVHSPILSTWIRVTIRIPVSHPLTFRAPRAHTVVGDLLELHCESLRGSP 411
QY 595 PILYFYHEDVTLGSSAPSGGASFNLSLTAHSGNYSCEANGLVAQHSIDTISLSVIV 654
Db 412 PILYFYHEDVTLGNSAPSGGASFNLSLTAHSGNYSCEADNGLGAQHSIGVSLRVTV 471
QY 655 PVSRLPILTFRAPRAQAVVGDLLELHCEALRGSSPILYFYHEDVTLGKISAPSGGGASFN 714
Db 472 PVSRLPILTRAPGAQAVVGDLLELHCESLRGSPILYFYHEDVTLGNIHSAHSGGGASFN 531
QY 715 LSLTTEHSGIYSCAENGLRAQRSEMTLKVAGEWALPTSSTSEN 759
Db 532 LSLTTEHSGNYSCEADNGLGAQHSKVTLNVTGLNVTG-----TSRN 568
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RESULT 14	
ADM35238	
ID	ADM35238 standard; protein; 734 AA.
XX	
AC	ADM35238;
XX	
XX	
DT	03-JUN-2004 (first entry)
XX	
XX	Human LY1448P cancer related protein for cancer detection method.
DE	
XX	
XX	cytostatic; T-cell vaccine; detection; cancer;
KW	chronic lymphocytic leukemia.
KW	
XX	
OS	Homo sapiens.
XX	
PN	WO2003077836-A2.
XX	
XX	
PD	25-SEP-2003.
XX	
PF	06-NOV-2002; 2002WO-US035728.
XX	
XX	06-NOV-2001; 2001US-00040862.
PR	

The present sequence is that of the novel human immunoglobulin receptor, immunoglobulin superfamily receptor translocation associated protein 3 (IRTA3), an Fc receptor involved in the pathogenesis of lymphoma and melanoma. Efforts to identify genes involved in chromosomal aberrations affecting band Ig21 in multiple myeloma and B cell lymphoma led to the discovery of IRTA1 and IRTA2 (see AAB82312-15) as founding members of a novel subfamily of related receptors within the immunoreceptor family. 3 additional proteins, IRTA3, IRTA4 and IRTA5 (see AAB82316-18), were subsequently identified, which are also members of this novel subfamily. The IRTA genes display a specific pattern of expression in mature B cells. IRTA3 is expressed in GC centrocytes and in perifollicular cells, which may include lymphoblasts and memory cells. This is analogous to IRTA2 expression. The invention provides IRTA nucleic acids and proteins, and antibodies directed to an epitope of an IRTA protein. Methods are claimed for: detecting a B cell malignancy comprising a Ig21 chromosomal rearrangement using a nucleic acid molecule that specifically hybridises with a unique sequence of human IRTA1-5; and treating a subject having a B cell cancer by administering an anti-IRTA antibody or an antisense oligonucleotide that specifically hybridises to IRTA mRNA so as to prevent overexpression of IRTA protein and hence to arrest cell growth or induce cell death of cancer cells expressing IRTA. The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma, multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse large cell lymphoma and follicular lymphoma. The B cell lymphoma is selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-Hodgkin's lymphoma

Sequence 734 AA;

Query Match 35.5%; Score 1417.5; DB 4; Length 734;
Best Local Similarity 41.6%; Pred. No. 1.9e-82;
Matches 318; Conservative 71; Mismatches 173; Indels 203; Gaps 10;

1 MLLWVILLVIAVPVSGQFARTPRPIITFLOPPTWTTPQGERVLTTCGFRFYSPQ-KTKWYH 59

Search completed: May 4, 2005, 11:32:51
Job time : 100.809 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:27:40 ; Search time 25.4304 Seconds
(without alignments)
2227.987 Million cell updates/sec

Title: US-09-724-254A-44
Perfect score: 3993
Sequence: 1 MLLWVILLVLPVSGQFART.....MVLKVGAEWALPTSSTSEN 759

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3792.5	95.0	1248	4	US-09-949-016-10595
2	3792.5	95.0	1248	4	US-09-949-016-10596
3	386	9.7	261	4	US-09-245-764-7
4	369.5	9.3	4391	4	US-10-006-011A-2
5	317.5	8.0	1709	4	US-09-949-016-10503
6	305.5	7.7	254	2	US-08-667-939A-3
7	305.5	7.7	254	2	US-08-433-123-3
8	304.5	7.6	254	2	US-08-667-939A-2
9	304.5	7.6	254	4	US-08-433-123-2
10	296.5	7.4	738	3	US-08-478-208-32
11	296.5	7.4	738	4	US-09-336-536-73
12	293	7.3	233	2	US-08-667-939A-6
13	293	7.3	233	4	US-08-433-123-6
14	292.5	7.3	254	2	US-08-667-939A-9
15	292.5	7.3	254	4	US-08-433-123-9
16	292	7.3	233	2	US-08-667-939A-5
17	292	7.3	233	2	US-08-667-939A-8
18	292	7.3	233	4	US-08-433-123-5
19	292	7.3	233	4	US-08-433-123-8
20	290	7.3	315	4	US-09-949-016-11121
21	290	7.3	315	4	US-09-949-016-11122
22	288.5	7.2	254	2	US-08-667-939A-4
23	288.5	7.2	254	4	US-08-433-123-4
24	286	7.2	233	2	US-08-667-939A-7
25	286	7.2	233	4	US-08-433-123-7
26	285.5	7.2	254	2	US-08-667-939A-1
27	285.5	7.2	254	4	US-08-433-123-1

28	285.5	7.2	738	6	5264554-2	Patent No. 5264554
29	285.5	7.2	738	6	5264554-2	Patent No. 5264554
30	280.5	7.0	698	2	US-08-602-725-36	Sequence 36, Appl
31	280.5	7.0	702	4	US-09-949-016-6484	Sequence 6484, Ap
32	280.5	7.0	734	2	US-08-389-459A-17	Sequence 17, Appl
33	280.5	7.0	734	3	US-08-987-867A-17	Sequence 17, Appl
34	280.5	7.0	740	4	US-09-949-016-8168	Sequence 8168, Ap
35	275	6.9	197	3	US-08-788-954-2	Sequence 2, Appl
36	275	6.9	203	2	US-08-667-939A-20	Sequence 20, Appl
37	275	6.9	203	4	US-08-433-123-20	Sequence 20, Appl
38	274	6.9	174	4	US-09-245-764-8	Sequence 8, Appl
39	271	6.8	215	2	US-08-667-939A-18	Sequence 18, Appl
40	271	6.8	215	4	US-08-433-123-18	Sequence 18, Appl
41	269.5	6.7	199	2	US-08-768-964-12	Sequence 12, Appl
42	269.5	6.7	199	3	US-09-005-299-12	Sequence 12, Appl
43	269.5	6.7	199	3	US-09-515-431-12	Sequence 12, Appl
44	269.5	6.7	263	2	US-08-768-964-2	Sequence 2, Appl
45	269.5	6.7	263	3	US-09-005-299-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-949-016-10595
; Sequence 10595, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT FILING DATE: 2000-04-14
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10595
; LENGTH: 1248
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10595

Query Match	95.0%	Score	3792.5;	DB 4;	Length	1248;
Best Local Similarity	97.1%;	Pred. No.	0;			
Matches	726;	Conservative	0;	Mismatches	1;	Gaps 2;
QY	1	MLLWVILLVLPVSGQFARTPRIIIFLOPWTTFVQGERVTLTKGFRFYSPOKTKYHR	60			
Db	476	MLLWVILLVLPVSGQFARTPRIIIFLOPWTTFVQGERVTLTKGFRFYSPOKTKYHR	535			
QY	61	YLKKEILRETPDNILEVQESGEYRCQAQSPVHLDFSSASLILOAPLSVPEGDSVV	120			
Db	536	YLKKEILRETPDNILEVQESGEYRCQAQSPVHLDFSSASLILOAPLSVPEGDSVV	595			
QY	121	LRCRAEAVTLNNTIYKNDNVLAFLNKRDTFPHIACLDKNGAYRCTGYKESCCPVSSNT	180			
Db	596	LRCRAEAVTLNNTIYKNDNVLAFLNKRDTFPHIACLDKNGAYRCTGYKESCCPVSSNT	655			
QY	181	VKIQVEPFRPVLRASSQPIISGNPVTLTCTQLSLERSDVLRRFRFRDDOTLGLWS	240			
Db	656	VKIQVEPFRPVLRASSQPIISGNPVTLTCTQLSLERSDVLRRFRFRDDOTLGLWS	715			
QY	241	LSPNFOITAMWSKDSGYFCKAATMPHSVSDSPRSWIQVQIPASHVPLVTLSPKALNFE	300			
Db	716	LSPNFOITAMWSKDSGYFCKAATMPHSVSDSPRSWIQVQIPASHVPLVTLSPKALNFE	775			
QY	301	GTKVTLHCQEDSLRFLRYFYHEGVLRHKSVCERGASISFSLTTENSNGYYCTADNG	360			

181 VKIQVCEPFRPVRASSFQISGNPVTILTCETQLSLERSDVLPRFRFRDDQDTLGLGWS 240
 656 VKIQVCEPFRPVRASSFQISGNPVTILTCETQLSLERSDVLPRFRFRDDQDTLGLGWS 715
 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIOVQIPASHVPLTSLPEKALNFE 300
 716 LSPNFQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIOVQIPASHVPLTSLPEKALNFE 775
 301 GTKVTLHCETOEDSLRTLYRFYHEGVPLRHKSVCRCERGASISFSLTTTENSNGNYCTADNG 360
 776 GTKVTLHCETOEDSLRTLYRFYHEGVPLRHKSVCRCERGASISFSLTTTENSNGNYCTADNG 835
 361 LGAKPSKAVSLSVTPVSHPVNLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
 836 LGAKPSKAVSLSVTPVSHPVNLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 895
 421 LERRSANSAGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTPVSHPVNLNLS 480
 896 LERRSANSAGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTPVSHPVNLNLS 955
 481 EALTFCGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGNY 540
 956 EALTFCGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGNY 1015
 541 CTADNGFGPQRSVSVLFTVTPVSRPILTLRVPRQAQVVGDLLELHCEAPRGSPPILYWF 600
 1016 CTADNGFGPQRSVSVLFTVTPVSRPILTLRVPRQAQVVGDLLELHCEAPRGSPPILYWF 1073
 601 YHEDVTLGSSAPSGGSEAFNLSLTAHSGNYSCEANNGLVQAHSDDTISLSVIVPVSRI 660
 1074 YHEDVTLGSSAPSGGSEAFNLSLTAHSGNYSCEANNGLVQAHSDDTISLSVIVPVSRI 1133
 661 LTRAPRAQAVVGDLLELHCEALRGSPPILYWFYHEDVTLGKISAPSGGSEAFNLSL 720
 1134 LTRAPRAQAVVGDLLELHCEALRGSPPILYWFYHEDVTLGKISAPSGGSEAFNLSL 1174
 721 HSGIYSCDADNGLEAQRSEMVTLKVAGE 748
 1175 HSGIYSCDADNGLEAQRSEMVTLKVAGE 1202

RESULT 3
 US-09-245-764-7
 ; Sequence 7, Application US/09245764
 ; Patent No. 6675105
 ; GENERAL INFORMATION:
 ; APPLICANT: Hogarth, P. Mark
 ; APPLICANT: Powell, Maree S.
 ; APPLICANT: McKenzie, Ian F.C.
 ; APPLICANT: Maxwell, Kelly F.
 ; APPLICANT: Garrett, Thomas P.J.
 ; APPLICANT: Epa, Vidana
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF FC RECEPTORS
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: 4102-4
 ; CURRENT APPLICATION NUMBER: US/09/245,764
 ; EARLIER FILING DATE: 1999-02-05
 ; EARLIER APPLICATION NUMBER: 60/099,994
 ; EARLIER FILING DATE: 1998-09-11
 ; EARLIER APPLICATION NUMBER: 60/073,972
 ; EARLIER FILING DATE: 1998-02-06
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 261
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-245-764-7

Query Match 9.7%; Score 386; DB 4; Length 261;
 Best Local Similarity 35.7%; Pred. No. 3.8e-26;
 Matches 95; Conservative 40; Mismatches 121; Indels 10; Gaps 6;

776 GTKVTLHCETOEDSLRTLYRFYHEGVPLRHKSVCRCERGASISFSLTTTENSNGNYCTADNG 835
 361 LGAKPSKAVSLSVTPVSHPVNLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
 836 LGAKPSKAVSLSVTPVSHPVNLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 895
 421 LERRSANSAGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTPVSHPVNLNLS 480
 896 LERRSANSAGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTPVSHPVNLNLS 955
 481 EALTFCGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGNY 540
 956 EALTFCGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGNY 1015
 541 CTADNGFGPQRSVSVLFTVTPVSRPILTLRVPRQAQVVGDLLELHCEAPRGSPPILYWF 600
 1016 CTADNGFGPQRSVSVLFTVTPVSRPILTLRVPRQAQVVGDLLELHCEAPRGSPPILYWF 1073
 601 YHEDVTLGSSAPSGGSEAFNLSLTAHSGNYSCEANNGLVQAHSDDTISLSVIVPVSRI 660
 1074 YHEDVTLGSSAPSGGSEAFNLSLTAHSGNYSCEANNGLVQAHSDDTISLSVIVPVSRI 1133
 661 LTRAPRAQAVVGDLLELHCEALRGSPPILYWFYHEDVTLGKISAPSGGSEAFNLSL 720
 1134 LTRAPRAQAVVGDLLELHCEALRGSPPILYWFYHEDVTLGKISAPSGGSEAFNLSL 1174
 721 HSGIYSCDADNGLEAQRSEMVTLKVAGE 748
 1175 HSGIYSCDADNGLEAQRSEMVTLKVAGE 1202

RESULT 2
 US-09-949-016-10596
 ; Sequence 10596, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO01307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10596
 ; LENGTH: 1248
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-949-016-10596

Query Match 95.0%; Score 3792.5; DB 4; Length 1248;
 Best Local Similarity 97.1%; Pred. No. 0;
 Matches 726; Conservative 0; Mismatches 1; Indels 21; Gaps 2;

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QY 20 TPRPIIFLQPPWTTVFOGERVTLTKGFRFYSPOKTKWYHYLGKEILRETPD---NILE 76
Db 1 TTKAVITLQPPWVSFOETVTLHCEVLHLPFGSSSTQWFVN--GTATQTSTPSYRITSAS 58
QY 77 VQESGEYRCOAQSGPLSPVHLDFSSASLILQAPLSVF--EGDSVWLRCAKAEVTLNNTI 135
Db 59 VNSGGEYRCORGSLGRSDPQLQELHGRGWLLOVSSRVFTGEPLALRCHAWKOKLVNVL 118
QY 136 YKNDNVLAFLNKRDTDFHIFACLNKGNGAYRCTGYKESCCPVSNTVKIOVOEPTFRPVL 195
Db 119 YRNGRKFKPFHNSNLTKTNISHNGTYHCSGMGXH--RYTSAGISVTVKELFPAPVLN 176
QY 196 ASSFOP--ISGNPVTLCETOLSLERSDVPLRFRFRDDQTLGLGWSLSPNQITAMWSD 254
Db 177 ASVTSPLLEGNLVTLSCETKLLQKQPLQLYFYFGMSKTL--RGRNTSSEYQILTARRED 235
QY 255 SGFYWCAATMPHSVSDSPRSWIOV 280
Db 236 SGLYWCEATDGNLKRSPLELOV 261

RESULT 4
US-10-006-011A-2
; Sequence 2, Application US/10006011A
; Patent No. 6821947
; GENERAL INFORMATION:
; APPLICANT: Iozzo, Renato V.
; TITLE OF INVENTION: Endorepellin: methods and compositions
; TITLE OF INVENTION: for inhibiting angiogenesis
; FILE REFERENCE: 8321-95
; CURRENT APPLICATION NUMBER: US/10/006,011A
; CURRENT FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4391
; TYPE: PRT
; ORGANISM: human
US-10-006-011A-2

Query Match 9.3%; Score 369.5; DB 4; Length 4391;
Best Local Similarity 22.9%; Pred. No. 9.4e-23;
Matches 190; Conservative 118; Mismatches 359; Indels 163; Gaps 39;

QY 23 PIIFLOPPWTTVQGERVTLTKGFRFYSPOK-TKWYHYLGKEILRETPDNL-----E 76
Db 2630 PPRIESSPTVVEGQTLDLNCVVAR--QPQALITWKRGSLPSRQTHGSHRLHOMS 2687

QY 77 VQESGEYRCOAQ-----GSP-----LSPVHLDFSSASLILQAPLSVF 114
Db 2688 VADSGEYVCRANNIDALEASIVISVSPSAGSPSPGSSMPIRIESSS-----HVA 2739

QY 115 EGDVSVLRCRAKAEVTLNNTIYKNDNVLA--FLNKRDTDFHIFACLNKGNGAYRC-----T 167
Db 2740 EGETDLNLCVPCQAHAQVTHWKRGGSLPSHHQTRGSRURLHHSVADSGEYVCRVWGS 2799

QY 168 GYKESCCPV---SSNTVKIOVOEPTFRPVLRL--ASSFQPTSGNPVTLC-----ETQLS 216
Db 2800 GPLEASVILVTIEASGSNAHVAPGAPPIRIEPPSSRVVAGQTLDLKCVPCQAHAQVT 2859

QY 217 LER--SDVPLRFRFRDDQTLGLGWSLSPNQITAMWSDSGFYWC-----AATMPHSV-- 269
Db 2860 WHKRGGNLPAHQVH-----GPLLRLNQVSPADSGEYSQVTSSTLEASVL 2907

QY 270 ISDPSRWIOVQIPASHPVLTLSPEKALNPEGKVTILHCBTQDSRLTYRFTHEG--VP 327
Db 2908 VTIEPSSPGPIAPGLAQPIYIEASSHVTGQTLDLNLCVPCQA--HAQVTWKRGSLP 2966

QY 328 LRHYSVRCERGASISFSLTT--ENSGNYCYCTADNGLGAKPSKAVSLSVTVPVSH----- 379
Db 2967 ARHQT-----HGSQRLHLVSPADSGEYVCRVWGS--PQEAFTVTVPPSGSSYRLR 3020

QY 380 -PVLNLSPPDLIFEGAKVTLHCEAQRGSLPILYQFHHDAALERRSANSAGVAISFSL 438
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Db 3021 SPVISIDPPESSTVQOQDASFCKLIHDGAPISLEWKTRNOLEDNVHISPNGSIIITVG 3080
QY 439 T-AEHSNGYVCTADNCGFGPORSKAVSLSIITVPVSHPVLTILSSAEALTFCGATVTLHCEVQ 497
Db 3081 TRFSNGHTVRCVASNAYGVAQS--VNLNVHGPTT--VSULPEGPVWVKVAVTLEC-VS 3136
QY 498 RGSPOILYQFHYEDMPLWS--SSTPSVGRVSFSLSLTEGH-----SGNYCYTA 543
Db 3137 AGEPR-----SSARWTRISSTPA-KLBQRTYGLMDSHAVLIQISSAKPSDAGTYVCLA 3187
QY 544 DNGFGPQORSEVSLFVTVPVSRPILTLRVPRAAV--GDLLHLCHEAPGSPILYW-- 599
Db 3188 QNALGTAQKQVEVIVDTGAMAPQVQAEAEALTVEAGHTATLRCSATGSPAPTTHWSK 3247
QY 600 -----FYHEDVTLCGSSAPSGEASFNLSLTAEHSNGYSCAEANGLVAQHS-D-TLSLV 652
Db 3248 LRSPLPWQR-----LEGDTLIIIPRAQODSGQYICNATS--PAGHAETIILHV 3295
QY 653 IVPVSRPILTFRAPRAQAVVGDILLELHCEALRGSSPLY-WFYHEDVTLCGISAPSGGA 711
Db 3296 ESP---PYATTVPEHASVQAGETVQLQCLA-HCTPPLTFQW-----SRVGSLLPGRA 3343
QY 712 SFNLSL-----TTEHSGIYSCADNGLGAEQRSEMVTLCVAGEWALPTSS 755
Db 3344 TARNELLHFERAAPEDSGRYCRVTKVNGVSAEFAQLLVQGGPPGSLPATS 3393

RESULT 5
US-09-949-016-10503
; Sequence 10503, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10503
; LENGTH: 1709
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10503

Query Match 8.0%; Score 317.5; DB 4; Length 1709;
Best Local Similarity 22.7%; Pred. No. 9.4e-19;
Matches 205; Conservative 88; Mismatches 362; Indels 249; Gaps 40;

QY 16 QPARTERPPI-IFLQPPWTTVFOGERVTLTKGFRFY-SPOKTKWYHYLGKEILRETPDN 73
Db 233 QVKYAPKGVKILLSPSGRNILPGELVTLTCQVNSSYPVSSIKW-----LKDGVRLQTKG 288
QY 74 ILEV-----QESGEYRCQAQ---GSPLSPPVHLDFSSASLILQAPLSVFEQDSVWLRCA 125
Db 289 VLHLPOAASDAGVYTCQAENGVSLSVSPISLHIFAEVQVSPAGPILNQVTLVCNT 348
QY 126 --KAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLNKGNGAYRCT-----GYKESCCPVSS 178
Db 349 PNEAPSDRLYSWYKNHVLLEDAHSHT-LRLHLATRADTGFYCFCEVQNVHGSER-----S 401
QY 179 NTVKIOVOEPTFRPVLRASSFQIPISGNPVTICE-----TQLSERSDVPLRFRFRDD 232
Db 402 GPVSVVNVNHPPLTPVLTA-FLEQAGLVGLHCISVSVSEPLATLVLSHGHLASTSGSDS 460
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TELEFAX: 202-737-3528
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 254 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-433-123-3

Query Match 7.7%; Score 305.5; DB 4; Length 254;
 Best Local Similarity 32.9%; Pred. No. 5.6e-19;
 Matches 91; Conservative 37; Mismatches 102; Indels 47; Gaps 11;
 QY 1 MLLWVILLVAPVSGOFARTPRPIIFLOPPWTTVFOGERVTLTKCGFRFYSPQ--KTKWY 58
 DB 4 LLLPTALLLVASGMRTEDLPKAVVLEPQWRYVLEKDSVTLKCG--AYSPEDNSTQWF 61
 QY 59 HRYLKGKILRETPDNILE-----VQESGEYRCQAQGSPLSPVHLDFSSASLI 106
 DB 62 HK-----ENLISSQASSYFIDAATVDDSGEYRCQTNLTSLSDPVQLEVQVCGWLL 110
 QY 107 LQAPLSVF-EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRTHDFHIFHACIKONGAY 164
 DB 111 LQAPRWVFKEDPIHLRCHSWKNTALHKVTYLONGKDKRYFHNSDFHIFKATLKDSGSY 170
 QY 165 RCTGYKESCCPVSNVTVKIQVQEPFTRPVLRRASSFQISGNPVTLCETOLSLSERSDVPL 224
 DB 171 FCRLGVCS-KNVSETVNIITQGLA--VSTISFFP-PGYQVSF-CLVWVLLFAVDT-- 223
 QY 225 RFRFRDDQTLGLGWSLSPNFQITAMWSKDSGFYCK 261
 DB 224 -----GLYFSVKTNIRSTRDKDHFCKWK 249

RESULT 8

US-08-667-939A-2
 Sequence 2, Application US/08667939A
 Patent No. 5998166
 GENERAL INFORMATION:
 APPLICANT: LUO, Shun
 TITLE OF INVENTION: CD16-II VARIANTS
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/667,939A
 FILING DATE: 24-JUN-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/433,123
 FILING DATE: 03-MAY-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: BROWDY, Roger L.
 REGISTRATION NUMBER: 25,618
 REFERENCE/DOCKET NUMBER: LUO-2A
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 254 amino acids
 TYPE: amino acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-667-939A-2

Query Match 7.6%; Score 304.5; DB 2; Length 254;
 Best Local Similarity 32.9%; Pred. No. 6.8e-19;
 Matches 91; Conservative 38; Mismatches 101; Indels 47; Gaps 11;
 QY 1 MLLWVILLVAPVSGOFARTPRPIIFLOPPWTTVFOGERVTLTKCGFRFYSPQ--KTKWY 58
 DB 4 LLLPTALLLVASGMRTEDLPKAVVLEPQWRYVLEKDSVTLKCG--AYSPEDNSTQWF 61
 QY 59 HRYLKGKILRETPDNILE-----VQESGEYRCQAQGSPLSPVHLDFSSASLI 106
 DB 62 HK-----ENLISSQASSYFIDAATVDDSGEYRCQTNLTSLSDPVQLEVQVCGWLL 110
 QY 107 LQAPLSVF-EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRTHDFHIFHACIKONGAY 164
 DB 111 LQAPRWVFKEDPIHLRCHSWKNTALHKVTYLONGKDKRYFHNSDFHIFKATLKDSGSY 170
 QY 165 RCTGYKESCCPVSNVTVKIQVQEPFTRPVLRRASSFQISGNPVTLCETOLSLSERSDVPL 224
 DB 171 FCRLGVCS-KNVSETVNIITQGLA--VSTNSFFP-PGYQVSF-CLVWVLLFAVDT-- 223
 QY 225 RFRFRDDQTLGLGWSLSPNFQITAMWSKDSGFYCK 261
 DB 224 -----GLYFSVKTNIRSTRDKDHFCKWK 249

RESULT 9

US-08-433-123-2
 Sequence 2, Application US/08433123
 Patent No. 6444789
 GENERAL INFORMATION:
 APPLICANT: LUO, Shun
 TITLE OF INVENTION: CD16-II VARIANTS
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/433,123
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: BROWDY, Roger L.
 REGISTRATION NUMBER: 25,618
 REFERENCE/DOCKET NUMBER: LUO-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 254 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-433-123-2

Query Match 7.6%; Score 304.5; DB 4; Length 254;
 Best Local Similarity 32.9%; Pred. No. 6.8e-19;

Matches 91; Conservative 38; Mismatches 101; Indels 47; Gaps 11;
 QY 1 MLLWVILVLPVSCQPARTPPIIFLOPPHTVFOGSRVTLCTCKGRFFYSPO--KTKWY 58
 Db 4 LLLPALLILVAGWRTDELKPAVVFLEPQWVLEKSDSVTLKCG--AKSPENSTQWP 61
 QY 59 HRYLKGELRTPDNILE-----VOESGEYRCQAQSPPLSSPVHLDFSSASLI 106
 Db 62 HK-----ENLISQASSYFIDAATVDDSGEYRCOTNLSTLSDPVQLEVQVGWLL 110
 QY 107 LQAPLSVF-EGDSVVLRCRAKAEVTLNNIY-KDNVLAFLNKRTDFH PHACLKONGAY 164
 Db 111 LQAPRVFKEEDPIHLRCHSWKNTALHKVTYLONGKDRKYFHNSDPHIPKATLKOSGY 170
 QY 165 RCTGYKESCCPVSSNTVKIOVEPTRPVLRRASSFPQISGNPVTLCETQLSLERSDVPL 224
 Db 171 FCKGLVGS-KNVSSETVNITIIQGLA--VSTNSFFP-PGVQVSF-CLVMVLLFAVDI-- 223
 QY 225 RFRFRDDQTLGLGWSLSPNFQITAMWSKDSGFYWK 261
 Db 224 -----GLYFVKTNIRSTRDKWOKHFKWRK 249

RESULT 10
 US-08-478-208-32
 ; Sequence 32, Application US/08478208A
 ; Patent No. 6087331
 ; GENERAL INFORMATION:
 ; APPLICANT: Newman, Peter J.
 ; APPLICANT: Kirschbaum, Nancy
 ; TITLE OF INVENTION: THERAPEUTIC USE OF PLATELET-ENDOTHELIAL CELL ADHESION
 ; TITLE OF INVENTION: MOLECULE-1 COMPOSITIONS
 ; FILE REFERENCE: 160180.90147
 ; CURRENT APPLICATION NUMBER: US/08/478,208A
 ; CURRENT FILING DATE: 1995-06-07
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 32
 ; LENGTH: 738
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-08-478-208-32

Query Match 7.4%; Score 296.5; DB 3; Length 738;
 Best Local Similarity 22.9%; Pred. No. 1.9e-17;
 Matches 136; Conservative 107; Mismatches 251; Indels 101; Gaps 26;
 QY 203 SGNPVTLCETQLSLERSDVPL-RFRFRDDQTLGLGWSLSPNFQITAMWSK----- 253
 Db 49 NGKNLTLOCFADVSTTSHVKPQHOMLFYKDDVLF-----YNISSMKSTESYFIPEV 99
 QY 254 ---DSGFYWKCAATMPHSVSDSPRSWIQV-----IPASHPVLTLSPKALNPEGTQVT 305
 Db 100 RYDSGTGYKTV-----IVNNKKTAEYQLLVGVPS--PRVTLDDKKEAI--OGGIVR 149
 QY 306 LHCETQEDSLRFLRFYHGVPLRHSVRCERGA-----ISFSLTTN----- 349
 Db 150 VNCSPVEE--KAPIHFTTEKLELNKMWKLKREKSRDQNFVLEFFVEQDRLVSPRCQ 207
 QY 350 ----SGNYCTADNGLGAKPKAVSLSVTPVSHPVNLNLSPELIFEGAKVTLHCEAQR 405
 Db 208 ARIISGIIHQWTS-----TKSELVTVTESFSTPKFHI-SPTGMIMEGAQLHIKCTIQV 260
 QY 406 GSL-----PILYQFHEDAAI--ERRSANSAGGVAISFSLTAHSGNYCTADNFGFQR 458
 Db 261 THLAQEFPEIITQ--KKAIVAHNRHGNKA---VYSVMVMEHSGNTCKVES---RI 311
 QY 459 SKAVSLSTVTPVSHPVNLTLSSAEALTFEGATVTLHCEVQGRSPQILYOFYHEDMPLWSSS 518
 Db 312 SKVSSIVNITELFSKPELESFTHLDQGERLNLSCSIP-GAPPANFTIQEDTIV--SQ 368
 QY 519 TPSVGRVFSFSLTEGHSNYCTADNFGFQRSEVSLFVTPVSRPILTLRVPRQAQV 578
 Db 368 QY 422

Db 369 TDQFTKIA-----SKSDSGTYICTAGIDKVKVKSNTVQIVVCEMLSQPRISYDA-QFEVI 422
 QY 579 VGDLLHCEAPRGSPPILYWFYHEDVTLTGSSASPGGEASFNLSLTAEHSGNYSCAANN 638
 Db 423 KGQTIIEVRCEISGTLPISYQLLTKTSKVLNSTKNSNDPAVFKDNPTD--VEYQCVADN 480
 QY 639 --GLVAQHSDDTSLSVIVVSPRILTFRAPRAQAVVGDLLHCEALRGSSPILYWFYHE 696
 Db 481 CHSHAKMLSEVLKRVIAPVDEVOISILSKV-VESGEDIVLQCAVNEGSGITKYFYRE 539
 QY 697 DVTILGKISAPSGGASG--NLSLTTEHSGIYSC-----EADNGLEAQRSEMTLKV 745
 Db 540 KEGKPFQMTSNATQAFWTKQKASKQEGEYCTAFNRAHASSVPSRKILTVRV 594

RESULT 11
 US-09-336-536-73
 ; Sequence 73, Application US/09336536
 ; Patent No. 6406884
 ; GENERAL INFORMATION:
 ; APPLICANT: Leiby, K.
 ; APPLICANT: McKay, C.
 ; APPLICANT: Bossone, S.
 ; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
 ; FILE REFERENCE: 7853-144
 ; CURRENT APPLICATION NUMBER: US/09/336,536
 ; CURRENT FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 73
 ; LENGTH: 738
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-336-536-73

Query Match 7.4%; Score 296.5; DB 4; Length 738;
 Best Local Similarity 22.9%; Pred. No. 1.9e-17;
 Matches 136; Conservative 107; Mismatches 251; Indels 101; Gaps 26;
 QY 203 SGNPVTLCETQLSLERSDVPL-RFRFRDDQTLGLGWSLSPNFQITAMWSK----- 253
 Db 49 NGKNLTLOCFADVSTTSHVKPQHOMLFYKDDVLF-----YNISSMKSTESYFIPEV 99
 QY 254 ---DSGFYWKCAATMPHSVSDSPRSWIQV-----IPASHPVLTLSPKALNPEGTQVT 305
 Db 100 RYDSGTGYKTV-----IVNNKKTAEYQLLVGVPS--PRVTLDDKKEAI--OGGIVR 149
 QY 306 LHCETQEDSLRFLRFYHGVPLRHSVRCERGA-----ISFSLTTN----- 349
 Db 150 VNCSPVEE--KAPIHFTTEKLELNKMWKLKREKSRDQNFVLEFFVEQDRLVSPRCQ 207
 QY 350 ----SGNYCTADNGLGAKPKAVSLSVTPVSHPVNLNLSPELIFEGAKVTLHCEAQR 405
 Db 208 ARIISGIIHQWTS-----TKSELVTVTESFSTPKFHI-SPTGMIMEGAQLHIKCTIQV 260
 QY 406 GSL-----PILYQFHEDAAI--ERRSANSAGGVAISFSLTAHSGNYCTADNFGFQR 458
 Db 261 THLAQEFPEIITQ--KKAIVAHNRHGNKA---VYSVMVMEHSGNTCKVES---RI 311
 QY 459 SKAVSLSTVTPVSHPVNLTLSSAEALTFEGATVTLHCEVQGRSPQILYOFYHEDMPLWSSS 518
 Db 312 SKVSSIVNITELFSKPELESFTHLDQGERLNLSCSIP-GAPPANFTIQEDTIV--SQ 368
 QY 519 TPSVGRVFSFSLTEGHSNYCTADNFGFQRSEVSLFVTPVSRPILTLRVPRQAQV 578
 Db 368 QY 422

Db 481 CHSHAKMLSEVLRVKVIAPVDEVOISILSSKV-VESGEDIVLQCAVNEGSGPIYKFYRE 539
Qy 697 DVTILGKISAPSGGASF--NLSLTHSHGIYSC----EADNGLEAQRSEMVTLKV 745
Db 540 KEGKPPQMTSNATQATFWTKQKASKEQEGEYCTAFNRANHASSVPSPSKILTTRV 594

RESULT 12

US-08-667-939A-6
; Sequence 6, Application US/08667939A
; Patent No. 5998166
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,939A
; FILING DATE: 24-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-667-939A-6

Query Match 7.3%; Score 293; DB 2; Length 233;
Best Local Similarity 34.7%; Pred. No. 6.3e-18;
Matches 84; Conservative 32; Mismatches 92; Indels 34; Gaps 10;
Qy 1 MLLWVILLVLAPVSGQFARTPRPIIFLOPWTTFVQGERVTLCKGPRFYSPQ--KTKWY 58
Db 4 LLLPTALLLVLSAGMRTEPLKAVFLEPQWYRVLEKDSVTLKCG--AYSPEDNSTQWF 61
Qy 59 HRYLGKILRETPDNILE-----VQSSGEYRCQAQGSPLSSPVHLDFSSASLI 106
Db 62 HN-----ENLISSQASSYFIDAATVDSGEYRCQTNLSTLSDPVQLEHVHVGWLL 110
Qy 107 LQAPLSVF-EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRTPHIFACILKONGAY 164
Db 111 LQAPRWFKEDPIHLRCHSWKNTALHKVLYLQNGDKRKYFHNSDFHIFKATLKDSGSY 170
Qy 165 RCTGYKESCCPVSNVTVKIQVQEPFTRPVLRASSFPISGNPVTLCETOLSERSDVPL 224
Db 171 FCRGLVGS-KNVSSETVNIITQGLA--VSTISSFSF-PGYQVSF-CLVMVLLFAVDGTGL 225
Qy 225 RF 226
Db 226 YF 227

RESULT 14

US-08-667-939A-9
; Sequence 9, Application US/08667939A
; Patent No. 5998166
; GENERAL INFORMATION:

RESULT 13
US-08-433-123-6
; Sequence 6, Application US/08433123
; Patent No. 6444789
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,123
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-433-123-6

Query Match 7.3%; Score 293; DB 4; Length 233;
Best Local Similarity 34.7%; Pred. No. 6.3e-18;
Matches 84; Conservative 32; Mismatches 92; Indels 34; Gaps 10;
Qy 1 MLLWVILLVLAPVSGQFARTPRPIIFLOPWTTFVQGERVTLCKGPRFYSPQ--KTKWY 58
Db 4 LLLPTALLLVLSAGMRTEPLKAVFLEPQWYRVLEKDSVTLKCG--AYSPEDNSTQWF 61
Qy 59 HRYLGKILRETPDNILE-----VQSSGEYRCQAQGSPLSSPVHLDFSSASLI 106
Db 62 HN-----ENLISSQASSYFIDAATVDSGEYRCQTNLSTLSDPVQLEHVHVGWLL 110
Qy 107 LQAPLSVF-EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRTPHIFACILKONGAY 164
Db 111 LQAPRWFKEDPIHLRCHSWKNTALHKVLYLQNGDKRKYFHNSDFHIFKATLKDSGSY 170
Qy 165 RCTGYKESCCPVSNVTVKIQVQEPFTRPVLRASSFPISGNPVTLCETOLSERSDVPL 224
Db 171 FCRGLVGS-KNVSSETVNIITQGLA--VSTISSFSF-PGYQVSF-CLVMVLLFAVDGTGL 225
Qy 225 RF 226
Db 226 YF 227

APPLICANT: LUO, Shun
TITLE OF INVENTION: C016-II VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,939A
FILING DATE: 24-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,123
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LUO-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-667-939A-9

Query Match 7.3%; Score 292.5; DB 2; Length 254;
Best Local Similarity 33.1%; Pred. No. 8e-18;
Matches 89; Conservative 38; Mismatches 111; Indels 31; Gaps 11;

Qy 1 MLLVILLVLAPVSGQFARTPRPIIFLQPPWTVFQGERVTLTCKGFRFYSPQ--KTKWY 58
Db 4 LLLPTALLLVASGMRTEDEPKAVVLEPQWYRVLEKDSVTLKCG--AYSPEDNSTQWF 61

Qy 59 HRYLGKEILRETPNII-----EVOESGEYRCQAGSPVHLDFFSSASLILOAPLSVF 114
Db 62 H---NESLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEVHIGWLLLOAPRWVF 118

Qy 115 -EGDSVVLRCFAKAEVTLNNTIY-KNDNVLAFLNKRDTDFHPIHACKDNGAYRCTGYKES 172
Db 119 KEEDEPIHLRCHSWKNVTAHKVYLONGGRKYFHNSDFYIPKATLKDSGSYFCRGLFGS 178

Qy 173 CCPVSSNTVKIQVQEPFTRPVLRASSFQIPISGNPVTLTCTQLSLERSDVLPRFRFRDD 232
Db 179 -KNVSSEVTNITITQGLA--VSTISSFPF-PGYQVSF-CLVMVLLFAVDT----- 223

Qy 233 QTLGLGWSLSPNFQITAMWSKDSGFYWC 261
Db 224 ---GLYFSVKTNIRSTRDWDKDKFKWRK 249

Search completed: May 4, 2005, 11:55:34
Job time : 27.4304 secs

APPLICANT: LUO, Shun
TITLE OF INVENTION: C016-II VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,939A
FILING DATE: 24-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,123
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LUO-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-667-939A-9

Query Match 7.3%; Score 292.5; DB 2; Length 254;
Best Local Similarity 33.1%; Pred. No. 8e-18;
Matches 89; Conservative 38; Mismatches 111; Indels 31; Gaps 11;

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Qy 59 HRYLGKEILRETPNII-----EVOESGEYRCQAGSPVHLDFFSSASLILOAPLSVF 114
Db 62 H---NESLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEVHIGWLLLOAPRWVF 118

Qy 115 -EGDSVVLRCFAKAEVTLNNTIY-KNDNVLAFLNKRDTDFHPIHACKDNGAYRCTGYKES 172
Db 119 KEEDEPIHLRCHSWKNVTAHKVYLONGGRKYFHNSDFYIPKATLKDSGSYFCRGLFGS 178

Qy 173 CCPVSSNTVKIQVQEPFTRPVLRASSFQIPISGNPVTLTCTQLSLERSDVLPRFRFRDD 232
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Qy 233 QTLGLGWSLSPNFQITAMWSKDSGFYWC 261
Db 224 ---GLYFSVKTNIRSTRDWDKDKFKWRK 249

RESULT 15
US-08-433-123-9
; Sequence 9, Application US/08433123
; Patent No. 644789
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: C016-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300

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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:38:21 ; Search time 80.5296 Seconds
(without alignments)
3139.559 Million cell updates/sec

Title: US-09-724-254A-44
Perfect score: 3993
Sequence: 1 MLWVILLVLPVSGQFART.....MVLKVGAEWALPTSSTSEN 759

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3993	100.0	759	14	US-10-040-862-10460 Sequence 10460, A
2	3993	100.0	759	15	US-10-057-475B-10460 Sequence 10460, A
3	3993	100.0	759	15	US-10-154-884B-10460 Sequence 10460, A
4	3993	100.0	759	15	US-10-403-847-7 Sequence 7, Appli
5	3993	100.0	759	16	US-10-764-324-10460 Sequence 10460, A
6	3967.5	99.4	790	15	US-10-403-847-4 Sequence 4, Appli
7	3923	98.2	977	14	US-10-040-862-10462 Sequence 10462, A
8	3923	98.2	977	15	US-10-057-475B-10462 Sequence 10462, A
9	3923	98.2	977	15	US-10-154-884B-10462 Sequence 10462, A
10	3923	98.2	977	15	US-10-403-847-9 Sequence 9, Appli
11	3923	98.2	977	16	US-10-764-324-10462 Sequence 10462, A
12	3916	98.1	977	14	US-10-241-220-97 Sequence 97, Appl
13	2962	74.2	592	14	US-10-040-862-10461 Sequence 10461, A

14	2962	74.2	592	15	US-10-057-475B-10461	Sequence 10461, A
15	2962	74.2	592	15	US-10-154-884B-10461	Sequence 10461, A
16	2962	74.2	592	15	US-10-403-847-8	Sequence 8, Appli
17	2962	74.2	592	16	US-10-764-324-10461	Sequence 10461, A
18	1854	46.4	438	15	US-10-403-847-6	Sequence 6, Appli
19	1502	37.6	317	15	US-10-403-847-2	Sequence 2, Appli
20	1419.5	35.5	582	15	US-10-162-335-94	Sequence 94, Appl
21	1417.5	35.5	707	15	US-10-108-260A-4774	Sequence 4774, Ap
22	1417.5	35.5	734	14	US-10-040-862-10463	Sequence 10463, A
23	1417.5	35.5	734	15	US-10-057-475B-10463	Sequence 10463, A
24	1417.5	35.5	734	15	US-10-154-884B-10463	Sequence 10463, A
25	1417.5	35.5	734	16	US-10-764-324-10463	Sequence 10463, A
26	1417.5	35.5	734	17	US-10-948-518-137	Sequence 137, App
27	1400	35.1	727	17	US-10-473-519-20	Sequence 20, Appl
28	1064	26.6	639	16	US-10-408-765A-2410	Sequence 2410, Ap
29	900	22.5	181	16	US-10-363-829-286	Sequence 286, App
30	900	22.5	181	16	US-10-363-829-431	Sequence 431, App
31	884.5	22.2	327	15	US-10-363-616-458	Sequence 458, App
32	871.5	21.8	421	15	US-10-162-335-96	Sequence 96, Appl
33	871.5	21.8	421	15	US-10-162-335-98	Sequence 98, Appl
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35	868.5	21.8	508	15	US-10-057-475B-10464	Sequence 10464, A
36	868.5	21.8	508	15	US-10-154-884B-10464	Sequence 10464, A
37	868.5	21.8	508	15	US-10-154-884B-11039	Sequence 11039, A
38	868.5	21.8	508	16	US-10-764-324-10464	Sequence 10464, A
39	868.5	21.8	508	17	US-10-948-518-119	Sequence 119, App
40	864.5	21.7	445	15	US-10-154-884B-11043	Sequence 11043, A
41	851.5	21.3	421	15	US-10-162-335-100	Sequence 100, App
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43	826.5	20.7	515	15	US-10-057-475B-10459	Sequence 10459, A
44	826.5	20.7	515	15	US-10-154-884B-10459	Sequence 10459, A
45	826.5	20.7	515	16	US-10-764-324-10459	Sequence 10459, A

ALIGNMENTS

RESULT 1

- US-10-040-862-10460
- Sequence 10460, Application US/10040862
- Publication No. US20030078396A1
- GENERAL INFORMATION:
- APPLICANT: Gaiger, Alexander
- APPLICANT: Algate, Paul A.
- APPLICANT: Mannion, Jane
- APPLICANT: Retter, Marc
- APPLICANT: Corixa Corporation
- TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
- FILE REFERENCE: 014058-013520US
- CURRENT APPLICATION NUMBER: US/10/040, 862
- CURRENT FILING DATE: 2001-11-06
- PRIOR APPLICATION NUMBER: US 60/186,126
- PRIOR FILING DATE: 2000-03-01
- PRIOR APPLICATION NUMBER: US 60/190,479
- PRIOR FILING DATE: 2000-03-17
- PRIOR APPLICATION NUMBER: US 60/200,545
- PRIOR FILING DATE: 2000-04-27
- PRIOR APPLICATION NUMBER: US 60/200,303
- PRIOR FILING DATE: 2000-04-28
- PRIOR APPLICATION NUMBER: US 60/200,779
- PRIOR FILING DATE: 2000-04-28
- PRIOR APPLICATION NUMBER: US 60/200,999
- PRIOR FILING DATE: 2000-05-01
- PRIOR APPLICATION NUMBER: US 60/202,084
- PRIOR FILING DATE: 2000-05-04
- PRIOR APPLICATION NUMBER: US 60/206,201
- PRIOR FILING DATE: 2000-05-22
- PRIOR APPLICATION NUMBER: US 60/218,950
- PRIOR FILING DATE: 2000-07-14
- PRIOR APPLICATION NUMBER: US 60/222,903
- PRIOR FILING DATE: 2000-08-03
- PRIOR APPLICATION NUMBER: US 60/223,416

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QY 541 CTADNGFGPORSSEVSVLFTVPSRPTLTVRAQAQVAVGDLLEHCEAPRGSPILYWF 600
Db 541 CTADNGFGPORSSEVSVLFTVPSRPTLTVRAQAQVAVGDLLEHCEAPRGSPILYWF 600
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Db 601 YHEDVTLGSSSAPSGGASFNLSLTAHSGNYSCAANNGLVAQSDTISLTVPSVRPI 660
QY 661 LTPRAPRAQAVVGDLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT 720
Db 661 LTPRAPRAQAVVGDLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT 720
QY 721 HSGIYSCAADNGLEAQRSEMVTLKVAGEWALPTSSTSEN 759
Db 721 HSGIYSCAADNGLEAQRSEMVTLKVAGEWALPTSSTSEN 759

RESULT 3
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; Sequence 10460, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR FILING DATE: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
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; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-10460

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Best Local Similarity 100.0%; Pred. No. 6.5e-281;
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Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHAPHACLKONGAYRCTGYKESCCPVSSNT 180
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Db 181 VKIQVQEPFTRPVLRASSFQPIISGNPVTLTCTQLSLERSDVPURFFRDDQTLGLGWS 240
QY 241 LSPNFQITAMWSKDSGFYWCKAATMPHSHSVISDSPRSIIQVQIPASHPVLTLSPKALNFE 300
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Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPDLIFEGAKVTLHCEAQRGLPILYQPHHDA 420
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Db 721 HSGIYSCAADNGLEAQRSEMVTLKVAGEWALPTSSTSEN 759

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; Sequence 7, Application US/10403847
; Publication No. US20040030098A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLICE VARIANTS OF A HUMAN
; FILE REFERENCE: D0228 NP
; CURRENT APPLICATION NUMBER: US/10/403,847
; CURRENT FILING DATE: 2003-03-28
; PRIOR FILING DATE: U.S. 60/368,671
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: U.S. 60/371,420
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 156

APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
FILE REFERENCE: 014058-013520US
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US/10/040,862
PRIOR FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
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PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
Remaining Prior Application data removed - See File Wrapper or PALM.
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SOFTWARE: FastSeq for Windows Version 3.0
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LENGTH: 759
TYPE: PRT
ORGANISM: Homo sapiens
US-10-764-324-10460

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Best Local Similarity 100.0%; Pred. No. 6.5e-281;
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DB 1 MLLWVILLVAPVSGQFARTPRPIIFLQPPWTVTFQGERVTLTKGFRFPYSPQTKWYHR 60
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 7
LENGTH: 759
TYPE: PRT
ORGANISM: Homo sapiens
US-10-403-847-7

Query Match 100.0%; Score 3993; DB 15; Length 759;
Best Local Similarity 100.0%; Pred. No. 6.5e-281;
Matches 759; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDPHIFHACLDKNGAYRCTGYKESCCPVSSNT 180
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DB 301 GTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVCERGASISFSLTTSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTVVSHVPLNLSPEDLIFEGAKVTLHCEAQRGSPLILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTVVSHVPLNLSPEDLIFEGAKVTLHCEAQRGSPLILYQFHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGQPSKAVSLSITVPVSHVPLTILSSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGQPSKAVSLSITVPVSHVPLTILSSA 480
QY 481 EALTFFEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSPFSLTEGHSGNY 540
DB 481 EALTFFEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSPFSLTEGHSGNY 540
QY 541 CTADNGFGQPSKAVSLSITVPVSHVPLNLSPEDLIFEGAKVTLHCEAQRGSPLILYQFHEDAA 600
DB 541 CTADNGFGQPSKAVSLSITVPVSHVPLNLSPEDLIFEGAKVTLHCEAQRGSPLILYQFHEDAA 600
QY 601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYCEANGLVAQHSDDTISLIVVPSRPI 660
DB 601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYCEANGLVAQHSDDTISLIVVPSRPI 660
QY 661 LTFRAPRAQAVVGDLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT 720
DB 661 LTFRAPRAQAVVGDLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT 720
QY 721 HSGIYSCADNGLEAQRSEMTVLKAVGEWALPTSTSEN 759
DB 721 HSGIYSCADNGLEAQRSEMTVLKAVGEWALPTSTSEN 759

RESULT 5
US-10-764-324-10460
Sequence 10460, Application US/10764324
Publication No. US2004017539A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc

Db 481 EALTFEGATVTLHCEVORSPQILYQYFHEDMPLWSSSTPSVGRVSFSLTEHSGNYY 540
Qy 541 CTADNGFGPQSRSEVVSFVTPVPSRPILTLRVPRQAQVVGDLLELHCEAPRGSPPIIYWF 600
Db 541 CTADNGFGPQSRSEVVSFVTPVPSRPILTLRVPRQAQVVGDLLELHCEAPRGSPPIIYWF 600
Qy 601 YHEDVTLGSSSAPSGGASFNLSLTAEHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660
Db 601 YHEDVTLGSSSAPSGGASFNLSLTAEHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660
Qy 661 LTFRAPRAQAVVGDLLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720
Db 661 LTFRAPRAQAVVGDLLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720
Qy 721 HSGIYSCEADNGLEAQRSEMVTLKAVAGEWALPTSSTSEN 759
Db 721 HSGIYSCEADNGLEAQRSEMVTLKAVAGEWALPTSSTSEN 759
RESULT 6
US-10-403-847-4
; Sequence 4, Application US/10403847
; Publication No. US20040030098A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLIC VARIANTS OF A HUMAN
; CELL SURFACE PROTEIN WITH IMMUNOLOGOBULIN FOLDS, BGSSG AND BGSST
; FILE REFERENCE: D0228 NP
; CURRENT APPLICATION NUMBER: US/10/403,847
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: U.S. 60/368,671
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: U.S. 60/371,420
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 4
; LENGTH: 790
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-847-4
Query Match 99.4%; Score 3967.5; DB 15; Length 790;
Best Local Similarity 96.1%; Pred. No. 4.9e-279;
Matches 759; Conservative 0; Mismatches 0; Indels 31; Gaps 1;
Qy 1 MLLWVILLVAPVSGQPARTPRPIIFLQPPWTTVFQGERVTLCKGPRFYSPOKTKWYHR 60
Db 1 MLLWVILLVAPVSGQPARTPRPIIFLQPPWTTVFQGERVTLCKGPRFYSPOKTKWYHR 60
Qy 61 YLGEKILRETPDNILEVOESGEYRCQAQSGPLSPVHLDFSS----- 102
Db 61 YLGEKILRETPDNILEVOESGEYRCQAQSGPLSPVHLDFSSGPHAAQAVNELLGSS 120
Qy 103 -----ASLIQAPLSVFEQSDSVLCRAKAEVTLNNTYKNDNVLAFLNKR 149
Db 121 DLLTWSQSAGITASLIQAPLSVFEQSDSVLCRAKAEVTLNNTYKNDNVLAFLNKR 180
Qy 150 DFHHPHACLDNGAYRCTGYKSCCPVSNVTKIQVQEPTRPVLRASSFPQISGNPVT 209
Db 181 DFHHPHACLDNGAYRCTGYKSCCPVSNVTKIQVQEPTRPVLRASSFPQISGNPVT 240
Qy 210 TCETQLSLERSDVPLEFRFRDQTLGLGWSLSPNFQITAMWSKDSGFYWCKAATWPHSV 269
Db 241 TCETQLSLERSDVPLEFRFRDQTLGLGWSLSPNFQITAMWSKDSGFYWCKAATWPHSV 300
Qy 270 ISDPSRWIQVQIPASHPVLTLSPEKALNFEKTVTLHCETQEDSLRTLYRFYHEGVPLR 329
Db 301 ISDPSRWIQVQIPASHPVLTLSPEKALNFEKTVTLHCETQEDSLRTLYRFYHEGVPLR 360
Qy 330 HKSVRCRGASISFSLTTEHSGNYYCTADNGLEAKGAKSVLSVTPVPSHPVNLSSPED 389
Db 361 HKSVRCRGASISFSLTTEHSGNYYCTADNGLEAKGAKSVLSVTPVPSHPVNLSSPED 420

Qy 390 LIPEGAKVTLHCEAQRGSLPILYQYFHEDAALERRRSANSAGGVAISFSLTAHSGNYYCT 449
Db 421 LIPEGAKVTLHCEAQRGSLPILYQYFHEDAALERRRSANSAGGVAISFSLTAHSGNYYCT 480
Qy 450 ADNGFGPQSRKAVSLSTVPSHPVLTLSAEALTFEGATVTLHCEVORSPQILYQYF 509
Db 481 ADNGFGPQSRKAVSLSTVPSHPVLTLSAEALTFEGATVTLHCEVORSPQILYQYF 540
Qy 510 EDMPLWSSSTPSVGRVSFSLTEHSGNYYCTADNGFGPQSRSEVVSFVTPVPSRPI 569
Db 541 EDMPLWSSSTPSVGRVSFSLTEHSGNYYCTADNGFGPQSRSEVVSFVTPVPSRPI 600
Qy 570 LRVPRQAQVVGDLLELHCEAPRGSPPIYWFYHEDVTLGSSSAPSGGASFNLSLTAEHS 629
Db 601 LRVPRQAQVVGDLLELHCEAPRGSPPIYWFYHEDVTLGSSSAPSGGASFNLSLTAEHS 660
Qy 630 GNYSCAANGLVAQHSDTISLSVIVPSRPIIFRAPRAQAVVGDLLELHCEALRGSSPI 689
Db 661 GNYSCAANGLVAQHSDTISLSVIVPSRPIIFRAPRAQAVVGDLLELHCEALRGSSPI 720
Qy 690 LYWFYHEDVTLGKISAPSGGASFNLSLTTEHSGIYSCEADNGLEAQRSEMVTLKAVAGEW 749
Db 721 LYWFYHEDVTLGKISAPSGGASFNLSLTTEHSGIYSCEADNGLEAQRSEMVTLKAVAGEW 780
RESULT 7
US-10-040-862-10462
; Sequence 10462, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-01352005
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0

QY 481 EALTFFGATVTLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSPFSLTGHSGNYY 540
Db 481 EALTFFGATVTLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSPFSLTGHSGNYY 540
QY 541 CTADNGFGPORSSEVSLFVTVPSRPIILTLRVPRQAQAVVGDLLLEHCEAPRGSPPIIYWF 600
Db 541 CTADNGFGPORSSEVSLFVTVPSRPIILTLRVPRQAQAVVGDLLLEHCEAPRGSPPIIYWF 600
QY 601 YHEDVTLGSSSAPSGGSEASFNLSLTAHSGNYSCEANNGLVVAQHSDDTISLSVIVPVSRI 660
Db 601 YHEDVTLGSSSAPSGGSEASFNLSLTAHSGNYSCEANNGLVVAQHSDDTISLSVIVPVSRI 660
QY 661 LTRAPRAQAVVGDLLLEHCEALRGSPPIIYWFYHEDVTILGKISAPSGGASFNLSLTTTE 720
Db 661 LTRAPRAQAVVGDLLLEHCEALRGSPPIIYWFYHEDVTILGKISAPSGGASFNLSLTTTE 720
QY 721 HSGIYSCADNGLEAQRSEMWTLKVA 746
Db 721 HSGIYSCADNGLEAQRSEMWTLKVA 746
RESULT 9
US-10-154-884B-10462
; Sequence 10462, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10462
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-10462
Query Match 98.2%; Score 3923; DB 15; Length 977;
Best Local Similarity 100.0%; Pred. No. 1.1e-275;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPWTWTFQGERVTLTKGFRFYSPOKTKWYHR 60
Db 1 MLLWVILLVAPVSGQFARTPRPIIFLOPWTWTFQGERVTLTKGFRFYSPOKTKWYHR 60

QY 61 YLQKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVPEGDSVV 120
Db 61 YLQKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVPEGDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFH1PHACLKONGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFH1PHACLKONGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSFOPIISGNPVTLTCTETQLSLERSDVPVLRFRFFRDDQTLGLGWS 240
Db 181 VKIQVQEPFTRPVLRASSFOPIISGNPVTLTCTETQLSLERSDVPVLRFRFFRDDQTLGLGWS 240
QY 241 LSNFOITAMWSKDSGFYMCATMPHSV1SDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
Db 241 LSNFOITAMWSKDSGFYMCATMPHSV1SDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTLHCETOEDSLRTLRYFHYHEGVPLRHKSVRCERGASISFSLTTTENGNYCTADNG 360
Db 301 GTKVTLHCETOEDSLRTLRYFHYHEGVPLRHKSVRCERGASISFSLTTTENGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTVPSHPVNLNLSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Db 361 LGAKPSKAVSLSVTVPSHPVNLNLSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPORSKAVSLSTVPSHPVLTLSA 480
Db 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPORSKAVSLSTVPSHPVLTLSA 480
QY 481 EALTFFGATVTLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSPFSLTGHSGNYY 540
Db 481 EALTFFGATVTLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSPFSLTGHSGNYY 540
QY 541 CTADNGFGPORSSEVSLFVTVPSRPIILTLRVPRQAQAVVGDLLLEHCEAPRGSPPIIYWF 600
Db 541 CTADNGFGPORSSEVSLFVTVPSRPIILTLRVPRQAQAVVGDLLLEHCEAPRGSPPIIYWF 600
QY 601 YHEDVTLGSSSAPSGGSEASFNLSLTAHSGNYSCEANNGLVVAQHSDDTISLSVIVPVSRI 660
Db 601 YHEDVTLGSSSAPSGGSEASFNLSLTAHSGNYSCEANNGLVVAQHSDDTISLSVIVPVSRI 660
QY 661 LTRAPRAQAVVGDLLLEHCEALRGSPPIIYWFYHEDVTILGKISAPSGGASFNLSLTTTE 720
Db 661 LTRAPRAQAVVGDLLLEHCEALRGSPPIIYWFYHEDVTILGKISAPSGGASFNLSLTTTE 720
QY 721 HSGIYSCADNGLEAQRSEMWTLKVA 746
Db 721 HSGIYSCADNGLEAQRSEMWTLKVA 746
RESULT 10
US-10-403-847-9
; Sequence 9, Application US/10403847
; Publication No. US20040030098A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLIC VARIANTS OF A HUMAN
; TITLE OF INVENTION: CELL SURFACE PROTEIN WITH IMMUNOGLOBULIN FOLDS, BGS5G AND BGS5I
; FILE REFERENCE: D0228 NP
; CURRENT APPLICATION NUMBER: US/10/403,847
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: U.S. 60/368,671
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: U.S. 60/371,420
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-847-9

Thu May 5 15:11:02 2005

us-09-724-254a-44.rapb

Query Match 98.2%; Score 3923; DB 15; Length 977;
Best Local Similarity 100.0%; Pred. No. 1.1e-275;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFOGERTVLTCKGFRFYSPOKTKWYHR 60
DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFOGERTVLTCKGFRFYSPOKTKWYHR 60
QY 61 YLKEILRETPDNILEVOESGEYRCQAQGPLSPVHLDFSSASLILQAPLSVFEQDSVV 120
DB 61 YLKEILRETPDNILEVOESGEYRCQAQGPLSPVHLDFSSASLILQAPLSVFEQDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLKONGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLKONGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSFOPIISGNPVTLCETQLSLERSDVPRLFRFRDDQTLGLGWS 240
DB 181 VKIQVQEPFTRPVLRASSFOPIISGNPVTLCETQLSLERSDVPRLFRFRDDQTLGLGWS 240
QY 241 LSPNFOITAMWSKDSGFYWCKAATWPHSVISDSPRSMIQVQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFOITAMWSKDSGFYWCKAATWPHSVISDSPRSMIQVQIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTILHCETOEDSLRTLRYFRYHEGVPLRHKSVCERGASISFSLTTENSGNYCTADNG 360
DB 301 GTKVTILHCETOEDSLRTLRYFRYHEGVPLRHKSVCERGASISFSLTTENSGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQVGLLELHCEAPRGSPPILYWF 600
DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQVGLLELHCEAPRGSPPILYWF 600
QY 601 YHEDVTLGSSAPSGGASPNLSLTAEHSGNYCTADNGFGFQPSKAVSLSVTPVSHPVLTLSA 480
DB 601 YHEDVTLGSSAPSGGASPNLSLTAEHSGNYCTADNGFGFQPSKAVSLSVTPVSHPVLTLSA 480
QY 481 EALTTEGATVTLHCEVQSGPOILYQFYHEDMPLWSSSTPSVGRVSFSFSLTEGHSNYY 540
DB 481 EALTTEGATVTLHCEVQSGPOILYQFYHEDMPLWSSSTPSVGRVSFSFSLTEGHSNYY 540
QY 541 CTADNGFGFQPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQVGLLELHCEAPRGSPPILYWF 600
DB 541 CTADNGFGFQPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQVGLLELHCEAPRGSPPILYWF 600
QY 601 YHEDVTLGSSAPSGGASPNLSLTAEHSGNYCTADNGFGFQPSKAVSLSVTPVSHPVLTLSA 480
DB 601 YHEDVTLGSSAPSGGASPNLSLTAEHSGNYCTADNGFGFQPSKAVSLSVTPVSHPVLTLSA 480
QY 721 HSGIYSCADNGLAEQSRSEMTLKA 746
DB 721 HSGIYSCADNGLAEQSRSEMTLKA 746
RESULT 11
US-10-764-324-10462
; Sequence 10462, Application US/10764324
; Publication No. US20040175739A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10764,324
; PRIOR APPLICATION NUMBER: US/10/040,862

PRIOR FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
Remaining prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10462
LENGTH: 977
TYPE: PRT
ORGANISM: Homo sapiens
US-10-764-324-10462
Query Match 98.2%; Score 3923; DB 16; Length 977;
Best Local Similarity 100.0%; Pred. No. 1.1e-275;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFOGERTVLTCKGFRFYSPOKTKWYHR 60
DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFOGERTVLTCKGFRFYSPOKTKWYHR 60
QY 61 YLKEILRETPDNILEVOESGEYRCQAQGPLSPVHLDFSSASLILQAPLSVFEQDSVV 120
DB 61 YLKEILRETPDNILEVOESGEYRCQAQGPLSPVHLDFSSASLILQAPLSVFEQDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLKONGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHIFACLKONGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSFOPIISGNPVTLCETQLSLERSDVPRLFRFRDDQTLGLGWS 240
DB 181 VKIQVQEPFTRPVLRASSFOPIISGNPVTLCETQLSLERSDVPRLFRFRDDQTLGLGWS 240
QY 241 LSPNFOITAMWSKDSGFYWCKAATWPHSVISDSPRSMIQVQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFOITAMWSKDSGFYWCKAATWPHSVISDSPRSMIQVQIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTILHCETOEDSLRTLRYFRYHEGVPLRHKSVCERGASISFSLTTENSGNYCTADNG 360
DB 301 GTKVTILHCETOEDSLRTLRYFRYHEGVPLRHKSVCERGASISFSLTTENSGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQVGLLELHCEAPRGSPPILYWF 420
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QY 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGFQPSKAVSLSVTPVSHPVLTLSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGFQPSKAVSLSVTPVSHPVLTLSA 480
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QY 541 CTADNGFGFQPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQVGLLELHCEAPRGSPPILYWF 600
DB 541 CTADNGFGFQPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQVGLLELHCEAPRGSPPILYWF 600
QY 601 YHEDVTLGSSAPSGGASPNLSLTAEHSGNYCTADNGFGFQPSKAVSLSVTPVSHPVLTLSA 480
DB 601 YHEDVTLGSSAPSGGASPNLSLTAEHSGNYCTADNGFGFQPSKAVSLSVTPVSHPVLTLSA 480

Db 601 YHEDVTLGSSAPSGGASFNLSLTAHSGNYSCEANGLVAQHSDFISLVIIVPSRPI 660
Qy 661 LTFRAPRAQAVVGDLLHCEALRGSSPILYFWYHEDVTLGKISAPSGGASFNLSLTTE 720
Db 661 LTFRAPRAQAVVGDLLHCEALRGSSPILYFWYHEDVTLGKISAPSGGASFNLSLTTE 720
Qy 721 HSGIYSCDADNGLEAQRSEMVTLKVA 746
Db 721 HSGIYSCDADNGLEAQRSEMVTLKVA 746

RESULT 12
US-10-241-220-97
; Sequence 97, Application US/10241220
; Publication No. US20030148408A1
; GENERAL INFORMATION:
; APPLICANT: Prantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P50101-US
; CURRENT APPLICATION NUMBER: US/10/241,220
; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 97
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-241-220-97

Query Match 98.1%; Score 3916; DB 14; Length 977;
Best Local Similarity 99.9%; Pred. No. 3.5e-275;
Matches 745; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPOKTKWYHR 60
Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPOKTKWYHR 60
Qy 61 YLCKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLIIQAPLSVFEGDSVV 120
Db 61 YLCKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLIIQAPLSVFEGDSVV 120
Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHFIPHACLKONGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHFIPHACLKONGAYRCTGYKESCCPVSSNT 180
Qy 181 VKIQVEPFRPVLRASSFOPIISGNPVTLTCETQLSLERSDVLPRFRFRDDOTLGLGWS 240
Db 181 VKIQVEPFRPVLRASSFOPIISGNPVTLTCETQLSLERSDVLPRFRFRDDOTLGLGWS 240
Qy 241 LSPNFQITAMWSKDSGYWCCKAATPHSVISDSPRSNIQVQIPASHPVLTLSPEKALNFE 300
Db 241 LSPNFQITAMWSKDSGYWCCKAATPHSVISDSPRSNIQVQIPASHPVLTLSPEKALNFE 300
Qy 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTTENSNGNYCTADNG 360
Db 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVCERGASISFSLTTENSNGNYCTADNG 360
Qy 361 LGAKPSKAVSLSTVPSVSHVPLNLSPEDELIPEGAKVTLHCEAQRSLPLIYQFHEDAA 420
Db 361 LGAKPSKAVSLSTVPSVSHVPLNLSPEDELIPEGAKVTLHCEAQRSLPLIYQFHEDAA 420
Qy 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSTVPSVSHVPLTLSSA 480
Db 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSTVPSVSHVPLTLSSA 480

Qy 481 EALTFEATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
Db 481 EALTFEATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
Qy 541 CTADNGFGPORSEVSLFVTVPSRPIILTRVPRQAQVGDLLHCEAQRGSPILYWF 600
Db 541 CTADNGFGPORSEVSLFVTVPSRPIILTRVPRQAQVGDLLHCEAQRGSPILYWF 600
Qy 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDFISLVIIVPSRPI 660
Db 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDFISLVIIVPSRPI 660
Qy 661 LTFRAPRAQAVVGDLLHCEALRGSSPILYFWYHEDVTLGKISAPSGGASFNLSLTTE 720
Db 661 LTFRAPRAQAVVGDLLHCEALRGSSPILYFWYHEDVTLGKISAPSGGASFNLSLTTE 720
Qy 721 HSGIYSCDADNGLEAQRSEMVTLKVA 746
Db 721 HSGIYSCDADNGLEAQRSEMVTLKVA 746

RESULT 13
US-10-040-862-10461
; Sequence 10461, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10461
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-10461

Query Match 74.2%; Score 2962; DB 14; Length 592;
Best Local Similarity 98.6%; Pred. No. 3e-206;
Matches 564; Conservative 0; Mismatches 4; Indels 4; Gaps 1;

PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 10979
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10461
LENGTH: 592
TYPE: PRT
ORGANISM: Homo sapiens
US-10-057-475B-10461

Query Match 74.2%; Score 2962; DB 15; Length 592;
Best Local Similarity 98.6%; Pred. No. 3e-206;
Matches 564; Conservative 0; Mismatches 4; Indels 4; Gaps 1;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRFVSPQKTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRFVSPQKTKWYHR 60
QY 61 YLGKEILRETPDNILEVOESGEYRCQAQGSPLSPVHLDPSSASLILQAPLSVFEQDSVV 120
DB 61 YLGKEILRETPDNILEVOESGEYRCQAQGSPLSPVHLDPSSASLILQAPLSVFEQDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDHPHACLDKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDHPHACLDKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIOVQEPFTRPVLRASSFQPIISGNPVTLTCTQLSLERSDVLPRFRDDQTLGLGWS 240
DB 181 VKIOVQEPFTRPVLRASSFQPIISGNPVTLTCTQLSLERSDVLPRFRDDQTLGLGWS 240
QY 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVISDSPRSWIOVQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVISDSPRSWIOVQIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTLHCETOEDSLRTLRYFHEGVPLRHKSVRCERGASISFSLTTTENSNGNYCTADNG 360
DB 301 GTKVTLHCETOEDSLRTLRYFHEGVPLRHKSVRCERGASISFSLTTTENSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQVSLPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQVSLPILYQFHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
QY 481 EALTTEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGNY 540
DB 481 EALTTEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGNY 540
QY 541 CTADNGFGPQRSSEVSLFVT-----VPVSRPIL 568
DB 541 CTADNGFGPQRSSEVSLFVTGKCVLASHHPPL 572

RESULT 15
US-10-154-884B-10461
Sequence 10461, Application US/10154884B
Publication No. US2004000561A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc W.
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRFVSPQKTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRFVSPQKTKWYHR 60
QY 61 YLGKEILRETPDNILEVOESGEYRCQAQGSPLSPVHLDPSSASLILQAPLSVFEQDSVV 120
DB 61 YLGKEILRETPDNILEVOESGEYRCQAQGSPLSPVHLDPSSASLILQAPLSVFEQDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDHPHACLDKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDHPHACLDKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIOVQEPFTRPVLRASSFQPIISGNPVTLTCTQLSLERSDVLPRFRDDQTLGLGWS 240
DB 181 VKIOVQEPFTRPVLRASSFQPIISGNPVTLTCTQLSLERSDVLPRFRDDQTLGLGWS 240
QY 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVISDSPRSWIOVQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVISDSPRSWIOVQIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTLHCETOEDSLRTLRYFHEGVPLRHKSVRCERGASISFSLTTTENSNGNYCTADNG 360
DB 301 GTKVTLHCETOEDSLRTLRYFHEGVPLRHKSVRCERGASISFSLTTTENSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQVSLPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIPEGAKVTLHCEAQVSLPILYQFHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480
QY 481 EALTTEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGNY 540
DB 481 EALTTEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGNY 540
QY 541 CTADNGFGPQRSSEVSLFVT-----VPVSRPIL 568
DB 541 CTADNGFGPQRSSEVSLFVTGKCVLASHHPPL 572

RESULT 14
US-10-057-475B-10461
Sequence 10461, Application US/10057475B
Publication No. US20040002068A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Clapper, Jonathan David
APPLICANT: Wang, Aijun
APPLICANT: Ordonez, Nadia
APPLICANT: Carter, Lauren
APPLICANT: McNeill, Patricia Dianne
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-014402US
CURRENT APPLICATION NUMBER: US/10/057,475B
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01

;; TITLE OF INVENTION: Hematological Malignancies
;; FILE REFERENCE: 014058-013521US
;; CURRENT APPLICATION NUMBER: US/10/154,884B
;; CURRENT FILING DATE: 2002-05-23
;; PRIOR APPLICATION NUMBER: US 60/186,126
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: US 60/190,479
;; PRIOR FILING DATE: 2000-03-17
;; PRIOR APPLICATION NUMBER: US 60/200,545
;; PRIOR FILING DATE: 2000-04-27
;; PRIOR APPLICATION NUMBER: US 60/200,303
;; PRIOR FILING DATE: 2000-04-28
;; PRIOR APPLICATION NUMBER: US 60/200,779
;; PRIOR FILING DATE: 2000-04-28
;; PRIOR APPLICATION NUMBER: US 60/200,999
;; PRIOR FILING DATE: 2000-05-01
;; PRIOR APPLICATION NUMBER: US 60/202,084
;; PRIOR FILING DATE: 2000-05-04
;; PRIOR APPLICATION NUMBER: US 60/206,201
;; PRIOR FILING DATE: 2000-05-22
;; PRIOR APPLICATION NUMBER: US 60/218,950
;; PRIOR FILING DATE: 2000-07-14
;; PRIOR APPLICATION NUMBER: US 60/222,903
;; PRIOR FILING DATE: 2000-08-03
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 11290
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 10461
;; LENGTH: 592
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-154-884B-10461

Query Match 74.2%; Score 2962; DB 15; Length 592;
Best Local Similarity 98.6%; Pred. No. 3e-206;
Matches 564; Conservative 0; Mismatches 4; Indels 4; Gaps 1;
QY 1 MLLWLIVLLVAPVSGQFARTPRPIIFLQPPWTVFQGERVTLCKGFRFYSPQKWKYHR 60
Db 1 MLLWLIVLLVAPVSGQFARTPRPIIFLQPPWTVFQGERVTLCKGFRFYSPQKWKYHR 60
QY 61 YLGEKILRETPDNLLEVOESGEYRCQAQGSPLSPVHLDFFSSASLILOAPLSVFEQDSVV 120
Db 61 YLGEKILRETPDNLLEVOESGEYRCQAQGSPLSPVHLDFFSSASLILOAPLSVFEQDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTFPHACLKONGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTFPHACLKONGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVEPPTPRVLRASSFQPIISGNPVTLTCTQLSLERSDVLPRFRFDDQTLGLWS 240
Db 181 VKIQVEPPTPRVLRASSFQPIISGNPVTLTCTQLSLERSDVLPRFRFDDQTLGLWS 240
QY 241 LSPNFQITAMWSKDSGYWCKAATMHSVTSDSRSHIQVQIPASHPVLTLSPEKALNPE 300
Db 241 LSPNFQITAMWSKDSGYWCKAATMHSVTSDSRSHIQVQIPASHPVLTLSPEKALNPE 300
QY 301 GTKVTLHCETQEDSLRTLRYFHEGVPLRHKSVRCERGASISFSLTTENSGNYCTADNG 360
Db 301 GTKVTLHCETQEDSLRTLRYFHEGVPLRHKSVRCERGASISFSLTTENSGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHVPLNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Db 361 LGAKPSKAVSLSVTPVSHVPLNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420
QY 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSTVPSHPVLTLSA 480
Db 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSTVPSHPVLTLSA 480
QY 481 EALTTFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
Db 481 EALTTFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540

Qy 541 CTADNGFGPORSSEVVSFLFTV----VPVSRPIL 568
Db 541 CTADNGFGPORSSEVVSFLFTVTKCWLASHPPPL 572
Search completed: May 4, 2005, 12:01:21
Job time : 83.5296 secs

RESULT 4
A46480
Fc gamma (IgG) receptor high affinity - mouse
N:Alternate names: high affinity IgG receptor
C:Species: Mus musculus (house mouse)
C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A46480; A43511
R:Osman, N.; Kozak, C.A.; McKenzie, I.F.; Hogarth, P.M.
J. Immunol. 148, 1570-1575, 1992
A:Title: Structure and mapping of the gene encoding mouse high affinity Fc gamma
A:Reference number: A46480; MUID:92166399; PMID:1531670
A:Accession: A46480
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-404 <OSM>
A:Cross-references: UNIPROT:P26151
A:Note: sequence extracted from NCBI backbone (NCBI:85205, NCBI:85208, NCBI:

RESULT 2

A39878

FC gamma (IgG) receptor I-A (high affinity) precursor - human

N:Alternate names: CD64

C:Species: Homo sapiens (man)

C:Date: 30-Dec-1991 #sequence revision 06-Sep-1996 #text_change 09-Jul-2004

C:Accession: A39878; I70304; B41357; S03018; I57525

R:van de Winkel, J.G.J.; Ernst, L.K.; Anderson, C.L.; Chiu, I.M.

J. Biol. Chem. 266, 13449-13455, 1991

A:Title: Gene organization of the human high affinity receptor for IgG, Fc gamma RI (CD64)

A:Reference number: A39878; MUID:91302383; PMID:1830050

A:Accession: A39878

A:Molecule type: DNA

A:Residues: 1-374 <UN>

A:Cross-references: UNIPROT:Q92663; GB:M63830; GB:M63835; NID:g180277; PIDN:AAA35678.1;

R:Porges, A.J.; Redecha, P.B.; Doebelle, R.; Pan, L.C.; Salmon, J.E.; Kimberly, R.P.

J. Clin. Invest. 90, 2102-2109, 1992

A:Title: Novel Fc gamma receptor I family gene products in human mononuclear cells.

A:Reference number: I55577; MUID:93055454; PMID:1430234

A:Accession: I70304

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-374 <RES>

A:Cross-references: GB:L03418; NID:g184840; PIDN:AAA36049.1; PID:g292169

R:Allen, J.M.; Seed, B.

Science 243, 378-381, 1989

A:Title: Isolation and expression of functional high-affinity Fc receptor complementary

A:Reference number: A41357; MUID:89100284; PMID:2911749

A:Accession: B41357

A:Molecule type: mRNA

A:Residues: 1-24,'S',26-337,'T',339-374 <ALI>

A:Cross-references: GB:X14356; GB:M21091; NID:g31331; PIDN:CAA32537.1; PID:g31332

R:Allen, J.M.; Seed, B.

Nucleic Acids Res. 16, 11824, 1988

A:Title: Nucleotide sequence of three cDNAs for the human high affinity Fc receptor (FCR

A:Reference number: S03018; MUID:89098339; PMID:2974947

A:Accession: S03018

A:Molecule type: mRNA

A:Residues: 1-24,'S',26-337,'T',339-374 <AL2>

A:Cross-references: EMBL:X14356; NID:g31331; PIDN:CAA32537.1; PID:g31332

R:Perez, C.; Wietzerbin, J.; Benach, P.D.

Mol. Cell. Biol. 13, 2182-2192, 1993

A:Title: Two cis-DNA elements involved in myeloid-cell-specific expression and gamma int

ism.

A:Reference number: I57525; MUID:93204964; PMID:8455606

A:Accession: I57525

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-8 <RE2>

A:Cross-references: GB:S57204; NID:g298692; PIDN:AAD13887.1; PID:g4261587

C:Genetics:

A:Gene: GDB:FCGR1A; CD64

A:Cross-references: GDB:I35911; OMIM:146760

A:Map position: 1q21-1q21

C:Superfamily: Fc gamma receptor I; immunoglobulin homology

C:Keywords: alternative splicing; glycoprotein; immunoglobulin receptor; transmembrane

F:1-15/Domain: signal sequence #status predicted <SIG>

F:16-292/Domain: extracellular #status predicted <EXT>

F:117-170/Domain: immunoglobulin homology <IMM2>

F:293-313/Domain: transmembrane #status predicted <TM>

F:59,78,152,159,163,195,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.5%; Score 418.5; DB 1; Length 374;

Best Local Similarity 37.0%; Pred. No. 6.1e-20;

Matches 108; Conservative 41; Mismatches 122; Indels 21; Gaps 10;

QY 1 MLLWILLVLAPVSGQFARTPRPIIFLOPPWTTVFGQSERVLTICKGRFYSPQTKWYHR 60

DB 7 LLLWV-----PVDQ-QVDTKAVITLQPPVSVFQETVTLHCEVLHPLGSSSTQWFLN 59

QY 61 YLIGKEILRETPD---NILEVQSGSYRCAQGSPLSSPVHLDFFSSASILLQAPLSVF--EG 116

R;Sears, D.W.; Osman, N.; Tate, B.; McKenzie, I.F.C.; Hogarth, P.M.
J. Immunol. 144, 371-378, 1990
A;Title: Molecular cloning and expression of the mouse high affinity Fc receptor for IgG
A;Reference number: A43511; MUID:90111035; PMID:2136886
A;Accession: A43511
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-404 <SEA>
A;Cross-references: GB:M31314; NID:g200752; PIDN:AAA40056.1; PID:g200753
C;Superfamily: Fc gamma receptor I; immunoglobulin homology
C;Keywords: immunoglobulin receptor; transmembrane protein
F;127-179/Domain: immunoglobulin homology <IMM>

Query Match 10.1%; Score 402.5; DB 2; Length 404;
Best Local Similarity 36.3%; Pred. No. 7.5e-19;
Matches 107; Conservative 42; Mismatches 131; Indels 15; Gaps 10;

QY 3 LWVI--LLVLAPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPOKTKWYHR 60
Db 10 MWLLTLLLVVPVGGVGNATKAVITLQPPWVIFQKENVTLWCEGPHLPDSDSTQWFN 69
QY 61 YLKGKILRETPDNL---EVOEGEYRCQAGSPLSPVHLDFSSASLILQAPLSVF-EG 116
Db 70 --GTAVQISTPSYSEAFQDSGEYRCQIGSSWSPDPVOLQIHNDWLLQASRRVLTEG 127
QY 117 DSVVLRCRA-KAEVTLNNTIYKNDNVLAFLNKRTHPHACLKONGAYRCTGYKESCCP 175
Db 128 EPLALRCHGKMKLVNVVYRNGKSFQF--SSDSEVAILKTNLSHGSIYHCSGTGRH--R 184
QY 176 VSNVTKIQVQEPFTRPVLRASSFOPI-SGNPVTLCETQLSRLSDVPLRFRFRDDQT 234
Db 185 YTSAGVSIYKELFTTPVLRASSVSSPPFEGSLVTLNCETNLLQLRPLQLHFFSYVGSKI 244
QY 235 LGLGWSLSPNFQITAMWSKDSGFYCKAATMPSHVSIDSRSWIOVIP-ASHPV 288
Db 245 LEYR-NTSEYHIAAREDRAGFYWCVEATEDSSVLKRSPELEQLVGLQSSAPV 298

RESULT 5
I48471
Fc gamma (IgG) receptor high affinity - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: I48471
R;Prins, J.B.; Todd, J.A.; Rodrigues, N.R.; Ghosh, S.; Hogarth, P.M.; Wicker, L.S.; Gaff
Science 260, 695-698, 1993
A;Title: Linkage on chromosome 3 of autoimmune diabetes and defective Fc receptor for Ig
A;Reference number: I48471; MUID:93242399; PMID:8480181
A;Accession: I48471
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-336 <RES>
A;Cross-references: EMBL:X70980; NID:g311748; PIDN:CAA50311.1; PID:g311749
C;Superfamily: Fc gamma receptor I; immunoglobulin homology
C;Keywords: immunoglobulin receptor
F;128-180/Domain: immunoglobulin homology <IMM>

Query Match 9.9%; Score 396; DB 2; Length 336;
Best Local Similarity 36.1%; Pred. No. 1.6e-18;
Matches 108; Conservative 43; Mismatches 130; Indels 18; Gaps 12;

QY 3 LWVI--LLVLAPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPOKTKWYHR 60
Db 10 MWLLTLLLVVPVGGVGNATKAVITLQPPWVIFQKENVTLWCEGPHLPDSDSTQWFN 69
QY 61 YLKGKILRETPD---NILEVOEGEYRCQAGSPLSPVHLDFSSAS-LILQAPLSVF-E 115
Db 70 --GTAVQISTPSYSEAFQDSGEYRCQIGSSWSPDPVOLQIHKEDWLLQASRRVLTE 127
QY 116 GDSVVLRCRA-KAEVTLNNTIYKNDNVLAFLNKRTHPHACLKONGAYRCTG---YKE 171
Db 128 GEPLALRCHGKMKLVNVVYRNGKSFQF--SSGSKIALKTNLSHGSIYHCSGMGRHY 186

QY 172 SCCPVSNTVKIQVQEPFTRPVLRASSFOPI-SGNPVTLCETQLSRLSDVPLRFRFR 230
Db 187 TSAGVSI-TVKAPPELFTTPVLRASSVSSPPFEGSLVTLNCETNLLQLRPLQLHFFSY 245
QY 231 DDQTLGLGWSLSPNFQITAMWSKDSGFYCKAATMPSHVSIDSRSWIOVIP-ASHPV 288
Db 246 GSKILEYR-NTSEYHIAAREDRAGFYWCVEATEDSSVLKRSPELEQLVGLQSSAPV 303

RESULT 6
A38096
perlecan precursor - human
N;Alternate names: basement membrane heparan sulfate proteoglycan; heparan sulfate proteo
C;Species: Homo sapiens (man)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 12-Jul-2004
A;Accession: A38096; S19256; S77946; A41059; A40306; B33625; A33625; A41736
R;Murdoch, A.D.; Dodge, G.R.; Cohen, I.; Tuan, R.S.; Iozzo, R.V.
J. Biol. Chem. 267, 8544-8557, 1992
A;Title: Primary structure of the human heparan sulfate proteoglycan from basement membr
tor, laminin, neural cell adhesion molecules, and epidermal growth factor.
A;Reference number: A38096; MUID:92235084; PMID:1569102
A;Accession: A38096
A;Molecule type: mRNA
A;Residues: 1-4391 <MUR>
A;Cross-references: UNIPROT:P98160; GB:M85289; NID:g184426; PIDN:AAA52700.1; PID:g184427
R;Kallunki, P.; Tryggvason, K.
J. Cell Biol. 116, 559-571, 1992
A;Title: Human basement membrane heparan sulfate proteoglycan core protein: a 467-kD pro
ell adhesion molecules, and epidermal growth factor.
A;Reference number: A41736; MUID:92112994; PMID:1730768
A;Accession: S19256
A;Molecule type: mRNA
A;Residues: 1-57, 'D', '59-434, 'A', '436, 'FL', '438-449, 'Q', '451-502, 'A', '503-792, 'K', '794-908, 'R',
71-2979, 'H', '2981-2994, 'G', '2996-3167, 'T', '3169-3240, 'R', '3242-3426, 'R', '3428-3631, 'Q', '3633-3
A;Cross-references: EMBL:X62515; NID:g29469; PIDN:CAA44373.1; PID:g29470
R;Kallunki, P.; Eddy, R.L.; Byers, M.G.; Kestilae, M.; Shows, T.B.; Tryggvason, K.
Genomics 11, 389-396, 1991
A;Title: Cloning of human heparan sulfate proteoglycan core protein, assignment of the g
A;Reference number: A41059; MUID:92120660; PMID:1685141
A;Accession: A41059
A;Molecule type: mRNA
A;Residues: 1-57, 'D', '59-434, 'A', '436, 'FL', '438-449, 'Q', '451-502, 'A', '503-792, 'K', '794-908, 'R',
71-2979, 'H', '2981-2994, 'G', '2996-3167, 'T', '3169-3240, 'R', '3242-3426, 'R', '3428-3631, 'Q', '3633-3
A;Cross-references: GB:S76436; NID:g243370; PIDN:AAB21121.1; PID:g243371
R;Dodge, G.R.; Kovalesky, I.; Chu, M.L.; Hassell, J.R.; McBride, O.W.; Yi, H.F.; Iozzo, F
Genomics 10, 673-680, 1991
A;Title: Heparan sulfate proteoglycan of human colon: partial molecular cloning, cellular
A;Reference number: A40306; MUID:91365376; PMID:1679749
A;Accession: A40306
A;Molecule type: mRNA
A;Residues: 1018-1405, 'G', '1407-1409, 'G', '1411-1465 <DOD>
A;Cross-references: GB:M64283; NID:g184424; PIDN:AAA52699.1; PID:g184425
R;Heremans, A.; van der Schueren, B.; De Cock, B.; Paulsson, M.; Cassiman, J.J.; van den
J. Cell Biol. 109, 3199-3211, 1989
A;Title: Matrix-associated heparan sulfate proteoglycan: core protein-specific monoclonal
A;Reference number: A33625; MUID:90078352; PMID:2687294
A;Accession: B33625
A;Molecule type: protein
A;Residues: 1379-1384, 'X', '1386-1388, 'X', '1390-1398 <HE2>
A;Accession: A33625
A;Molecule type: Protein
A;Residues: 2166-2171, 'X', '2173-2175, 'X', '2177-2185 <HE3>
A;Note: peptide potentially matches four different regions of sequence shown
C;Genetics:
A;Gene: GDB:HSPG2

A;Cross-references: GDB:126372; OMIM:142461
A;Map position: lp36.1-lp36.1
C;Keywords: chondroitin sulfate proteoglycan; glycoprotein; heparan sulfate; transmembrane
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-4391/Product: perlecan #status predicted <MAT>
F;22-193/Domain: I <DOM1>
F;194-530/Domain: II <DOM2>
F;199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;531-1676/Domain: III <DOM3>
F;1159-1206/Domain: laminin-type EGF-like homology <LEG>
F;1563-1610/Domain: laminin-type EGF-like homology <EG7>
F;1613-1668/Domain: laminin-type EGF-like homology <LEG>
F;1677-3686/Domain: IV <DOM4>
F;2007-2034/Domain: transmembrane #status predicted <TRM>
F;3687-4391/Domain: V <DOM5>
F;3845-3880/Domain: EGF homology <EGF1>
F;3888-3921/Domain: EGF homology <EGF>
F;3953-4106/Domain: laminin G repeat homology <LG2>
F;4147-4175/Domain: EGF homology <EGF2>
F;4149-4151/Region: motor neuron attachment (L-R-E) motif
F;4299-4301/Region: motor neuron attachment (L-R-E) motif
F;65,71,76/Binding site: heparan sulfate (Ser) (covalent) #status predicted
F;89,554,1755,2121,3072,3105,3279,3780,3836,4068/Binding site: carbohydrate (Asn) (coval)
F;2995,3933,4179/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted

Query Match 9.3%; Score 369.5; DB 2; Length 4391;
Best Local Similarity 22.9%; Pred. No. 2.5e-15;
Matches 190; Conservative 118; Mismatches 359; Indels 163; Gaps 39;

QY 23 PIIFLOPMTTVPQGRVLTCKGFRFYSPQK-TKWHRYLKEILRETPDNIL-----E 76
DB 2630 PPIRIESSPTVVEGQTLNLCVVAR--QPQAIITWYKGGSLPSRSHQTHGSLRLHQMS 2687

QY 77 VOSSGVRQAO-----GSP-----LSSPVHLPSSASLILOAPLSVF 114
DB 2688 VADSGEYVCRANNIDALEASIVISVPSAGSPSAPGSSMPRIESSSS-----HVA 2739

QY 115 EGDVSVLRCRAKAEVTLNNTIYKNDNLVA--FLNKRDTFHIHACLKONGYRC-----T 167
DB 2740 EGETDLNLCVQQAHAQVTHWKRGGSLPSHHQTRGSRLLHHVSPADSGEYVCRVMGSS 2799

QY 168 GYKESCCPV---SSNTVKIQVQPFTRPVLR--ASSFQIPISGNPVTLC-----ETQLS 216
DB 2800 GPLEASVLVTIETASGSSAVHPAPGAPPIRIEPPSSRVABGQTLDLKCVQQAHAQVT 2859

QY 217 LER--SDVPLRFRFRDDQTLGLGWSLSNFIQTAMWSDSGFYWCK-----AATMPHSV- 269
DB 2860 WHKRGNLPARHGVH-----GPLLRLNQVSPADSGEYSCQVTGSSGTLASVL 2907

QY 270 ISDSPRSWIQVQIPASHVPLTSPKALNPEGKVTILHCTQEDSLRTLYRFHFG--VP 327
DB 2908 VTIEPSSPGIPAPLAGAQTPIEASSHVTGQTLNLCVQQA--HAQVTWYKGGSLP 2966

QY 328 LRKSVRCERGASISFSLTT--ENSGNYCTADNGLGAKPSKAVSLSVTPVSH----- 379
DB 2967 ARHQT-----HGSQRHLNVPADSGEYVCRASGPG--PQEQASFTVTPPSGSSVRLR 3020

QY 380 -PVNLSSPDLIPEGAKVTLHCEAQRGSLPIIYQFHEDAAALERSANSAGGVAISFSL 438
DB 3021 SPVISIDPPSSTVQCGQDASFCLLHDGAAPISLEWTKRNOELEDNVHISPNGSIITVG 3080

QY 439 T-AHSGNYYCTADNGLGAKPSKAVSLSVTPVSHVPLTSSAEALTFFGATVTLHCEVQ 497
DB 3081 TRPSNHNCTYRCVASNAYGVAQS--VNLNVHSGPPT--VSVLPEGVVWVKVAVTLEC-VS 3136

QY 498 RGSPOILYQFVHEDMPLWS--SSTPSVGRVSFSLSLTEGH-----SGNYCTYA 543
DB 3137 AGEPR-----SSARWTRISSTPA-KLEORTYGLMDSHAVLIQISSAKPSDAGTVVCLA 3187

QY 544 DNGFGPQRSEVSLFVTPVSRPILTLRVPRAQAV--GDLLELHCEAPRGPSPILYW-- 599

Db 3188 QNALGTAQKQVEVIVDTGAMAPGAPQVQABEALTVAGHTATLRCSATGSPAPTIHWSK 3247
QY 600 -----FYHEDVTLGSSASGGEASNLSTLAHSGNYSCEANGLVAOHS-D-TISLSV 652
Db 3248 LRSPLPMQHR-----LEGDTLIIPRVAQDQSGYICNATS--PAGHAATILHV 3295
QY 653 IVPVSRPILTRAPRAQAVVGDLLLEHCEALRGSSPILY-WFYHEDVTLGKISAPSGGGA 711
Db 3296 ESP---PYATVPEHASVQAGETVQLQCLA-HGTPLPLTFQW-----SRVGSLLPGR 3343
QY 712 SFNLSL-----TTEHSGIYSCADNGLGAEARSEMVTILKVAGEWALPTSS 755
Db 3344 TARNELLHFERAAPEDSGRYCRVTNKVGSAAFAQLLVQGGPGLPATS 3393

RESULT 7
138346
elastic titin - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I38346
R;Label: S.; Kolmerer, B.
Science 270, 293-296, 1995
A;Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A;Reference number: A57430; MUID:96026330; PMID:7569978
A;Accession: I38346
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-7962 <RES>
A;Cross-references: UNIPROT:Q10465; EMBL:X90569; NID:gl017426; PIDN:CAA62189.1; PID:gl01:
C;Genetics:
A;Gene: GDB:TTN
A;Cross-references: GDB:I27867; OMIM:188840
A;Map position: 2q31-2q31

Query Match 8.7%; Score 347; DB 2; Length 7962;
Best Local Similarity 24.3%; Pred. No. 1.6e-13;
Matches 197; Conservative 100; Mismatches 156; Gaps 38;

QY 23 PIIFLOPMTTVPQGRVLTLC-----KGRFYSPQKTKWHRYLKEILRE 69
DB 216 PTFLSRPKSLTTFVGGKAAKFCITVGTPIETIWKDGAALSPSPNWRISDAENKHILEL 275

QY 70 TPDNILEVQESGEYRCQAGSPLSPVHLPDSSASLIL-----OAPLSVEGDSVV 120
DB 276 SN---LTIQDRGVYSCKA-----SNKFGADICQAEELIIDKPHFIKELEPVQSAINKKVH 327

QY 121 LECRA-----KAEVTLNNTIYK-----NDNVLAFLNKRDTFHIHACLKONGYRCITYKES 172
DB 328 LECQVDEDRKVTVTWWSKDGQKLPPGKYKICPEDKIATLEIPDLAKLQSGTYVCTASNEA 387

QY 173 CCPVSNVTVKIQVQPFTRPVLRASFPISGNPVTLCETQLSLERSDVLPRFRFRDD 232
DB 388 GSSSCSAITVREPPSPFKV--DPSYLMPLGESARLHCK-----LKGSPV-IQVTFWFKNN 440

QY 233 QTLGLGWSLSNPF-----QITAMWSDSGFYWCKAATMPHSHVISDSRSHIQVQIPAS 285
DB 441 KELSESNTVMYFVNSEAILDITDKVEDSGSYCEAV---NDVGSDDSCSTEIVIKPEPS 497

QY 286 HPVLTLSPEKALNPFRTKVTILHCT-----OEDSLRT--LYRFYHEGVPLRHK 331
DB 498 F-IKTELEPADIY--RGTNALLOCEVSGTGPFSEISWFKDKQIRSSKKYRLFQ-----K 548

QY 332 SVRCERGASISFSLTENSNGNYCTADNGLGAKPSKAVSLSVTPVSHVPLNLSPEDLI 391
DB 549 SLVCLC-----IFSNSADVGEYECVAVNEVGKCGCWATHL-----LKEPPTFVKVDDLI 599

QY 392 FEGAKVTLHCEAQRGSLPIL-----YQPHHEDAALERSANSAGGVAISF--SLTAHS 443
DB 600 ALGGQVTTLQAAVRGSEPISTVMKRGQEVIREDDGKIKMSFSN---GVAVLIIPTDQVQISFG 656

QY 444 GNYCTADNGLGFPQSRKAVSLSVTPVSHVPLTSSAEAL-TFEGATVTLHCEVQRGSPQ 502

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Db 657 GKYTCLAEAGSOTSVEI-----VKEPAKIERAELQVTDGDPATLEYTV-AGTPE 710
Qy 503 ILQFYHEDMPLSSSTPSVGRVSF-----SFLTEGH-SGNYCTADNGFGPQORSEV 554
Db 711 LKPKWYKDGRLVASKK--YRISFKNVAQLKEYSAELHDSGOYTFEISNEVSSCET 767
Qy 555 VSLFVTVVPSRPILTTLVRAQAVVGDLELHCEAPRGSPILYFWFHEDVTLGSSAPS 614
Db 768 TFTVLDRIA-PPTKPLRNVDSVVGTCRLDCKIAGSLPMRVSWF--KD---GKEIAAS 821
Qy 615 G-----GEASFN-LSLTAESGNYSCAENGLVAQHSDTISLIVIVPSRPILTFR 665
Db 822 DRTIAFVEGTASLEIIRVDMNDAGNFTCRATNSVSGKDS-----SGALIVQPPSPVTK 876
Qy 666 PRAQAVVGDLELHCEALRGSPIT-LYWFYHEDVTLGKISAPSGG-----ASFNL 715
Db 877 PGSKDVLPGSAVCKSTFGSTPLTIRWF-----KGNKELVSGGSGYITKEALESLEL 930
Qy 716 SLT-TEHSGIYSEADN---GLERQORSEMV 741
Db 931 YLVKTSDSGTYYTCKVSNVAGGVECSANLFV 960

RESULT 8
S18252
heparan sulfate proteoglycan - mouse
N;Alternate names: perlecan
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 12-Jul-2004
R;Accession: S18252; A31917; B31917; S66460
R;Noonan, D.M.; Fullle, A.; Valente, P.; Cai, S.; Horigan, E.; Sasaki, M.; Yamada, Y.; Ha
J. Biol. Chem. 266, 22939-22947, 1991
A;Title: The complete sequence of perlecan, a basement membrane heparan sulfate proteog
adhesion molecule.
A;Reference number: S18252; MUID:92078153; PMID:1744087
A;Accession: S18252
A;Molecule type: mRNA
A;Residues: 1-3707 <NO>
A;Cross-references: UNIPROT:Q05793; EMBL:M77174; NID:G200295; PIDN:AAA39911.1; PID:G2002
R;Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogeli, G.; Sasaki, M.; Yamada, Y.; Ha
J. Biol. Chem. 263, 16379-16387, 1988
A;Title: Identification of cDNA clones encoding different domains of the basement membra
A;Reference number: A92680; MUID:89034110; PMID:2972708
A;Accession: A31917
A;Molecule type: mRNA
A;Residues: 940-1601 <NO2>
A;Cross-references: GB:J04054; NID:G200252; PIDN:AAA39899.1; PID:G200253
A;Accession: B31917
A;Molecule type: mRNA
A;Residues: 1870-2600 <NO3>
A;Cross-references: GB:J04055; NID:G200300; PIDN:AAA39912.1; PID:G200301
R;Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.
Eur. J. Biochem. 231, 551-556, 1995
A;Title: Structural properties of recombinant domain III-3 of perlecan containing a glob
A;Reference number: S66460; MUID:95377282; PMID:7649154
A;Accession: S66460
A;Molecule type: protein
A;Residues: 1272-1274,'X', 1276,'X', 1278-1279 <SCH>
C;Keywords: glycoprotein
F;199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;764-811/Domain: laminin-type EGF-like homology <LEG>
F;1159-1206/Domain: laminin-type EGF-like homology <LEG7>
F;1563-1610/Domain: laminin-type EGF-like homology <LEG8>
F;1613-1668/Domain: laminin-type EGF-like homology <LEG9>
F;3163-3198/Domain: EGF homology <EGF>
F;3270-3293/Domain: laminin G repeat homology <LG2>
F;3464-3492/Domain: EGF homology <EGF7>
F;1256,1891,2336,2394,2427/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Query Match 8.4%; Score 336.5; DB 2; Length 3707;
Best Local Similarity 22.7%; Pred. No. 2.8e-13;
Matches 190; Conservative 100; Mismatches 365; Indels 183; Gaps 39;

Qy 23 PIIFLOPPWTTVQGERVTLTKGFRFPYSPQKT-----KWHYRVLGKEILRETPDNI 74
Db 1955 PRVOVGPRTQVHEGRTVRLYCRAAGVPSASITWRKEGGLPFRHQHAGRLRL-----HH 2010
Qy 75 LEVQESGEYRCQAQG-----SPLS-SPVHLDFFSSASLILQAPLS 112
Db 2011 MSVADSGEYVCRAANNIDAQETSIMISVSPSTNSPPAPAPIRIESSSS-----R 2062
Qy 113 VFEGDSVVLRCRAKAETVLTNNITYKNDNVLAFLNKR--TDFHPHACLKONGAYRC----- 166
Db 2063 VAEQGTLDLNCVVVPGHAHAQVTHKRGSLPHTHQTHGSLRLYLTVSSADSGEYVCSVLS 2122
Qy 167 -TCYKESCCPVSSNTVKIQVQEPFTRPVLRL--ASSFQIPISGNPVTITC-----ETQLSL 217
Db 2123 SSGPLEASVLVSIPTAAANVHIIPGVVPPPIRIETSSSRVABEGQTLDLSVVPQGAHAQVTV 2182
Qy 218 ERSDVPLRFRFRDDQTLGLGWSLSPNFOI-----TAMWSKDSGFYWCK-----AATMP 266
Db 2183 HKR-----GGSLPAGHVHGHMLRLNRVSPADSGEYSQVTCSSGTL 2225
Qy 267 HSVI-----SOSPRSWIQVIPA-----SHPVLTLSPEKALNFGTKVTLHCETQ-EDSLR 316
Db 2226 ASVLVTIEASEPSP-----IPAGLAQFVYIESSSHLT-EGQTVDLKCVVPGQAHAQ 2277
Qy 317 TLYRFHEGVLPHKSVRCERGASIS-FSLTTSNGNYCTADNGLGAKSKAVSLSVTV 375
Db 2278 VTWHKRGSLPARHQV-----HGSLLRLYLQSLPADSGEYVQCVAG--SSHEPEHAEFKLTV 2331
Qy 376 PVSH-----PVLNLSPEDLIFEGAKVTLHCEAQGSLPILYOFHHEDDAALERSAN 427
Db 2332 PSSQNSFRLSRPSVISIEPSSSTVQQQODASFCLTHEGAMPKVEWKIRDOLEDNVHI 2391
Qy 428 SAGGVAISF-----SLTAHSGNYCTADNGFGPQRSKAVSLSITVPVSHPVLTLSAEAL 483
Db 2392 SPNGSIITIVAPGPATMEPTA---CVASNVYGAQS-VVNLSVHGPT--VSVLPEGPVH 2445
Qy 484 TREGATVTLHCEVQORSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTSGH----- 535
Db 2446 VRMGKDITLEC-ISSGEPR-----SSPRMTRLGIPVKLEPRMFGLMNSHAMLKIASV 2496
Qy 536 ----SGNYCTADNGFGPORSVWVSLFV---TPVSRPILTLRVRAQAVVGDLELHCE 588
Db 2497 KPSDAGTYVCOAQNALGTAKQK-VELIVDTGTVPAGTQVQVESESLTLEAGHTATLHCS 2555
Qy 589 APRGSPILYFWFHEDVTLGSSAP-----SGGEASFNLSLTAHSGNYSCAENGLVA 642
Db 2556 ATGNPPPTIHW-----SKLRAPLPQWHRTEGNTLVIPRVAQDQSGQYICNATNS--A 2605
Qy 643 QHSD-TISLSVIVPSRPILTFRPRAQAVVGDLELHCEALRGSSPILY-WFYHEDVTL 700
Db 2606 GHTEATVVLVRESPP--PYATTIPEHTSAQGNLVQLQCLA-HGTPPLTYQW-----SLV 2656
Qy 701 GKISAPSGGGSFNLSL---TTEHSGIYSCAENGLAEQORSEMVTLLKAVGEWALPTSS 755
Db 2657 GGVLPEKAVVRNQLLEPTVPEDSGRYRCQVSNRVGSAEFAQVILVQSSSNLPDTS 2714

RESULT 9
I46021
Fc-gamma receptor II - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: I46021; S40204
R;Zhang, G.; Young, J.R.; Tregaskes, C.R.; Howard, C.J.
Immunogenetics 39, 423-427, 1994
A;Title: Cattle Fc gamma II: molecular cloning and ligand specificity.
A;Reference number: I46021; MUID:94245284; PMID:8188320
A;Accession: I46021
A;Status: preliminary; translated from GB/EMBL/DBJ
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A:Molecule type: mRNA
A:Residues: 1-296 <ZHA>
A:CROSS-references: UNIPROT:Q28110; EMBL:X75671; NID:G437978; PIDN:CAA53367.1; PID:G437978
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: immunoglobulin receptor

Query Match 8.2%; Score 326.5; DB 2; Length 296;
Best Local Similarity 37.0%; Pred. No. 4.5e-14;
Matches 90; Conservative 34; Mismatches 100; Indels 19; Gaps 10;

QY 1 MLLWILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRFYSPQKTKWYHR 60
DB 28 MLLWILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRFYSPQKTKWYHR 86
QY 61 YLKEI-LRETDPNILEV--QSGYRCQAQSGPLSSPVHLDFFSSASLILOAPLSV-EG 116
DB 87 --GSSHTKQPSYFRAGSNDGSGYRCQREQTSLSDPVHLDVSDWLLQTPSLVFOEG 144
QY 117 DSVLRCRAKAEVTLNN-TIYKNDNVLAFLNKRTPHACLDKNGAYRCTGYKESCCP 175
DB 145 EPIMLRCHSWRNOPLNKITFYQDRSKIPSYQRTNFSIPRAWLSHGQVHCTAFIGKMLH 204
QY 176 VSNVTVKIQVPPFTRPVLRASSFOIPISGNPVTL-TCETQLSLERSDVLPRFRFRDQOT 234
DB 205 --SQPNNITVQE-----SSSGPSSMTVAIGTCFAAIVAIAITW-FRLRRKDIS 254
QY 235 LGL 237
DB 255 AGL 257

RESULT 10
A34636
C:Species: Guinea pig
C:Superfamily: Cavia porcellus (guinea pig)
C:Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 16-Jul-1999
C:Accession: A34636
R:Tominaga, M.; Sakata, A.; Ohmura, T.; Yanashita, T.; Koyama, J.; Onoue, K.
Biochem. Biophys. Res. Commun. 168, 683-689, 1990
A:Title: The structure and expression of the guinea pig Fc receptor for IgG1 and IgG2 (Fc gamma receptor III; immunoglobulin homology)
A:Reference number: A34636; MUID:90241239; PMID:1692213
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-270 <TOM>
A:CROSS-references: GB:M35272
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: immunoglobulin receptor
F:37-88/Domain: immunoglobulin homology <IMM>

Query Match 8.0%; Score 319; DB 2; Length 270;
Best Local Similarity 35.6%; Pred. No. 1.2e-13;
Matches 84; Conservative 28; Mismatches 72; Indels 52; Gaps 8;

QY 1 MLLWILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRFYSPQKTKWYHR 60
DB 1 MLLWILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRFYSPQKTKWYHR 60
QY 61 YLKEI-LRETDPNILEV--QSGYRCQAQSGPLSSPVHLDFFSSASLILOAPLSV 113
DB 61 --GRLI----PTQVLPYRFTAKGNDGSGYRCQAQSGTSLSDPVRLDVISDWLVTQSLI 114
QY 114 F-EGDSVILCRKAEVTLNN-----TIYKNDNVLAFLNKRTPHACLDKNGAYRC 166
DB 115 FQEGDVILRCH-----SWNNPLAKVTFYHNGVAKYFISIKNFSIPQANHSHGAYNC 169
QY 167 TGYKESCCPVSSNTVKIQVPPFTRPVLRASSFOIPISGNPVTLTKCETQLSLERSDV 222
DB 170 TGL-----IGRTSHTSP-----PVTITVQGPXSSDSMW 198

RESULT 11
JH0371
B-cell adhesion protein CD22 beta splice form precursor - human
N:Alternate names: B-cell membrane protein CD22
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: JH0371; I56171
R:Wilson, G.L.; Fox, C.H.; Fauci, A.S.; Kehrl, J.H.
J. Exp. Med. 173, 137-146, 1991
A:Title: cDNA cloning of the B cell membrane protein CD22: a mediator of B-B cell interaction
A:Reference number: JH0371; MUID:91086838; PMID:1985119
A:Accession: JH0371
A:Molecule type: mRNA
A:Residues: 1-847 <WIL2>
A:CROSS-references: UNIPROT:O60926; GB:X59350; NID:G36090; PIDN:CAA42006.1; PID:G36091
A:Experimental source: B lymphocyte
A:Note: the authors translated the codon AAT for residue 358 as Met
R:Wilson, G.L.; Najfeld, V.; Kozlow, E.; Menniger, J.; Ward, D.; Kehrl, J.H.
J. Immunol. 150, 5013-5024, 1993
A:Title: Genomic structure and chromosomal mapping of the human CD22 gene.
A:Reference number: I56171; MUID:93267103; PMID:8496602
A:Accession: I56171
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 121-269, T' 271-473, K' 475-614, R' 616-638, Y' 640-711, 777-847 <WIL2>
A:CROSS-references: GB:S61375; NID:G385980; PIDN:AAC18956.1; PID:G3184492
C:Genetics:
A:Gene: GDB:CD22
A:CROSS-references: GDB:I27545; OMIM:107266
A:Map position: 19q13.1-19q13.1
A:Introns: 138/1; 240/1; 329/1; 417/1; 503/1; 591/1; 679/1; 711/2; 804/3
A:Keywords: alternative splicing; B-cell; cell adhesion; dimer; glycoprotein; phosphoprotein
F:1-19/Domain: signal sequence #status predicted <Sig>
F:20-847/Product: B lymphocyte cell adhesion protein #status predicted <MAT>
F:346-398/Domain: immunoglobulin homology <IMM1>
F:609-661/Domain: immunoglobulin homology <IMM2>
F:688-706/Domain: transmembrane #status predicted <TRA>
F:767,101,112,135,164,231,363,445,448,479,574,634/Binding site: carbohydrate (Asn) (covalent)
F:764,789/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 7.9%; Score 314.5; DB 2; Length 847;
Best Local Similarity 22.1%; Pred. No. 1.1e-12;
Matches 176; Conservative 116; Mismatches 326; Indels 177; Gaps 39;

QY 4 WLLLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFR-----FYSP 52
DB 7 WLLLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFR-----FYSP 52
QY 53 QKTWYHYLKGKILLRETPDNILEVOESGEYRCQAQSGPLSS-----PVHLDFSSASLI 106
DB 63 EYNKTSKFDGTRLYESTKDGKVP---PSEQKRVQFLGDKNKNCTLSIHPVHLN----- 112
QY 107 LQAPLSVFEQDSVVLRCRAKAEVTLNN-TIYKNDNVLAFLNKRTPHACLDKNGAYRC 155
DB 113 -----DSGQLGLRMESKTEKWMER-IHLNVSEPP-----PPIQLPPEIQESQ 155
QY 156 -----ACLKNDNGAYRCTGYKESCCPVSSNTVKIQVPPFTRPVLRASSFOIPISGNPVTLTC 211
DB 156 EYTLTCLLN---FSCYGY-----PIQLQ-----WLEGEVPMROAA 187
QY 212 ETQLSLERSDVLPRFRFRDQOTLGLWSLSPNFQITAMWSKDSGFYWCKAATPHSVIS 271
DB 188 VTSTSLTKSV-----FTFSE-----LKFSQWSHHGKIVTCQLQDADGKFLS 230
QY 272 DSPRSWIOVQIPASH-PVLTTL--SPEKALNFGTKVTLHCETQEDSLR-TLYRFYHEGVP 327
DB 231 ND-----TVQLNVKHTPKLEIKVTPSDAIVREGDSVTMTCEVSSSNPEYTVSMWKDGS 285
QY 328 LRHKSVCRCERASISPSL-----TTENSGNYCYCTADNGLGAKPKSKAVSLSVT-VPVSHVP 381
DB 286 LKKQN-----TFTMLREVTKDQSGKYCCQVNDVGPGRSESEVFLQVQAPESIV 336
QY 382 LNLSSPEDLIFEGAKVTLHCEAQRGSLPILYOFHHEDAALERRRANSAGVVAISLSLTA 441
DB 337 QILHSP---AVESQVEFLCMSLANPLPTNYTWYHNGEMQGRTEBK---VHIP-KILPW 389

A:Molecule type: mRNA
A:Residues: 1-296 <ZHA>
A:CROSS-references: UNIPROT:Q28110; EMBL:X75671; NID:G437978; PIDN:CAA53367.1; PID:G437978
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: immunoglobulin receptor

Query Match 8.2%; Score 326.5; DB 2; Length 296;
Best Local Similarity 37.0%; Pred. No. 4.5e-14;
Matches 90; Conservative 34; Mismatches 100; Indels 19; Gaps 10;

QY 1 MLLWILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRFYSPQKTKWYHR 60
DB 28 MLLWILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRFYSPQKTKWYHR 86
QY 61 YLKEI-LRETDPNILEV--QSGYRCQAQSGPLSSPVHLDFFSSASLILOAPLSV-EG 116
DB 87 --GSSHTKQPSYFRAGSNDGSGYRCQREQTSLSDPVHLDVSDWLLQTPSLVFOEG 144
QY 117 DSVLRCRAKAEVTLNN-TIYKNDNVLAFLNKRTPHACLDKNGAYRCTGYKESCCP 175
DB 145 EPIMLRCHSWRNOPLNKITFYQDRSKIPSYQRTNFSIPRAWLSHGQVHCTAFIGKMLH 204
QY 176 VSNVTVKIQVPPFTRPVLRASSFOIPISGNPVTL-TCETQLSLERSDVLPRFRFRDQOT 234
DB 205 --SQPNNITVQE-----SSSGPSSMTVAIGTCFAAIVAIAITW-FRLRRKDIS 254
QY 235 LGL 237
DB 255 AGL 257

RESULT 10
A34636
C:Species: Guinea pig
C:Superfamily: Cavia porcellus (guinea pig)
C:Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 16-Jul-1999
C:Accession: A34636
R:Tominaga, M.; Sakata, A.; Ohmura, T.; Yanashita, T.; Koyama, J.; Onoue, K.
Biochem. Biophys. Res. Commun. 168, 683-689, 1990
A:Title: The structure and expression of the guinea pig Fc receptor for IgG1 and IgG2 (Fc gamma receptor III; immunoglobulin homology)
A:Reference number: A34636; MUID:90241239; PMID:1692213
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-270 <TOM>
A:CROSS-references: GB:M35272
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: immunoglobulin receptor
F:37-88/Domain: immunoglobulin homology <IMM>

Query Match 8.0%; Score 319; DB 2; Length 270;
Best Local Similarity 35.6%; Pred. No. 1.2e-13;
Matches 84; Conservative 28; Mismatches 72; Indels 52; Gaps 8;

QY 1 MLLWILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRFYSPQKTKWYHR 60
DB 1 MLLWILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRFYSPQKTKWYHR 60
QY 61 YLKEI-LRETDPNILEV--QSGYRCQAQSGPLSSPVHLDFFSSASLILOAPLSV 113
DB 61 --GRLI----PTQVLPYRFTAKGNDGSGYRCQAQSGTSLSDPVRLDVISDWLVTQSLI 114
QY 114 F-EGDSVILCRKAEVTLNN-----TIYKNDNVLAFLNKRTPHACLDKNGAYRC 166
DB 115 FQEGDVILRCH-----SWNNPLAKVTFYHNGVAKYFISIKNFSIPQANHSHGAYNC 169
QY 167 TGYKESCCPVSSNTVKIQVPPFTRPVLRASSFOIPISGNPVTLTKCETQLSLERSDV 222
DB 170 TGL-----IGRTSHTSP-----PVTITVQGPXSSDSMW 198

RESULT 11
JH0371
B-cell adhesion protein CD22 beta splice form precursor - human
N:Alternate names: B-cell membrane protein CD22
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: JH0371; I56171
R:Wilson, G.L.; Fox, C.H.; Fauci, A.S.; Kehrl, J.H.
J. Exp. Med. 173, 137-146, 1991
A:Title: cDNA cloning of the B cell membrane protein CD22: a mediator of B-B cell interaction
A:Reference number: JH0371; MUID:91086838; PMID:1985119
A:Accession: JH0371
A:Molecule type: mRNA
A:Residues: 1-847 <WIL2>
A:CROSS-references: UNIPROT:O60926; GB:X59350; NID:G36090; PIDN:CAA42006.1; PID:G36091
A:Experimental source: B lymphocyte
A:Note: the authors translated the codon AAT for residue 358 as Met
R:Wilson, G.L.; Najfeld, V.; Kozlow, E.; Menniger, J.; Ward, D.; Kehrl, J.H.
J. Immunol. 150, 5013-5024, 1993
A:Title: Genomic structure and chromosomal mapping of the human CD22 gene.
A:Reference number: I56171; MUID:93267103; PMID:8496602
A:Accession: I56171
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 121-269, T' 271-473, K' 475-614, R' 616-638, Y' 640-711, 777-847 <WIL2>
A:CROSS-references: GB:S61375; NID:G385980; PIDN:AAC18956.1; PID:G3184492
C:Genetics:
A:Gene: GDB:CD22
A:CROSS-references: GDB:I27545; OMIM:107266
A:Map position: 19q13.1-19q13.1
A:Introns: 138/1; 240/1; 329/1; 417/1; 503/1; 591/1; 679/1; 711/2; 804/3
A:Keywords: alternative splicing; B-cell; cell adhesion; dimer; glycoprotein; phosphoprotein
F:1-19/Domain: signal sequence #status predicted <Sig>
F:20-847/Product: B lymphocyte cell adhesion protein #status predicted <MAT>
F:346-398/Domain: immunoglobulin homology <IMM1>
F:609-661/Domain: immunoglobulin homology <IMM2>
F:688-706/Domain: transmembrane #status predicted <TRA>
F:767,101,112,135,164,231,363,445,448,479,574,634/Binding site: carbohydrate (Asn) (covalent)
F:764,789/Binding site: phosphate (Thr) (covalent) #status predicted

R:Kershaw, J.
submitted to the EMBL Data Library, December 1994
A:Reference number: Z19929
A:Accession: T24734
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-5198 <W12>
A:Cross-references: EMBL:247070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b
A:Experimental source: clone T0999
C:Genetics:
A:Gene: him-4; F15G9.4b
A:Map position: X
A:Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
; 2512/2; 2933/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1;
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/1

Query Match 7.8%; Score 312; DB 2; Length 5198;
Best Local Similarity 21.6%; Pred. No. 1.7e-11;
Matches 186; Conservative 123; Mismatches 357; Indels 194; Gaps 43;

QY 14 SQCFARTPRPIIFLOPPWTTVQ-----GERVLTCKGFRFPYSPQTKWHRVYLKGEI 66
DB 687 AGQ-ARDTDLMLATPPKVEIIQNMVGRGDRVSFECKTIRGKPHKIRWFKN--GKDL 743
QY 67 LRETPDNILEVQ-----SGEYRCAQ--GSPSSPVHLDPFSSASLILQAPL 111
DB 744 IK--PDDYKINEGQHINGAKDEAGYSCVGENWAGKDV-QVANLSVGRVPTIIESPH 800
QY 112 SVFEG--DSVVLRCRA-----KAEV---TINNTIY---KNDNVLAFLNKRTRDFH 152
DB 801 TVRVNIERQVTLQCLAVGIPPPPEIEWQKGNVLLATLNNPRYTQADGNLL----- 850
QY 153 IPHACLKONGARCTGYKESCCPVSNSNTVKIQVEP-----FTRPVLK--ASSFQPISG 204
DB 851 ITDAQIEDQOQTC-----IARTYGOQSQTTLMTGLVSPFLGHVPPEQLLEG 901
QY 205 NPVTLTCTQLSLERSDVLPRFRFRDDOTGLGWSLSPNFOITAMS-----KDS 255
DB 902 QDLTSLSCVVLTGTPRSIV---WIKDDKPVVEG---PTIKIEGGSLRLRGNPKDE 953
QY 256 GFYCKAATMPSHVSIDSPSRWIQVQIP--ASHPVLTLSPKALNFEGT-----KVLHC 308
DB 954 GKYTCLIA-----VSPAGNSTLHINVQLIKKPEFYKPEGIVFKPTISGDMDEKHAVV 1006
QY 309 ETQESL-----RTLRFYHGVPLRHKSVRCERGASISFSLTEN----- 349
DB 1007 NSTHDVLDGEGFAIPCWSGTPPPPIITWYLDGRPTPN-----SRDFTVADNTLIV 1058
QY 350 -----SGNYCTADNGLGAKPSKAVSLSVTPVSHP-VLNLSSPEDLIFEGAKVTLHC 401
DB 1059 RADKSYSGVYTQATNSAGDNEOKTIRIMTPTMISPGSSFNWVDDLF-----TIPC 1113
QY 402 EAQROSLPILYQPHHEDAALRRSANSAGVAISFLSATAHSGNYYCTADNFGFQPSKA 461
DB 1114 DVYGDPKPI-TWLLDDKPFTEGVNEDGSLTIP-NVNEAHRGTFTCHAQNAAG-NDTRT 1170
QY 462 VSLSTIVPSHPVLTSLSSAALTFEGATVLTACEVQSGSPQILYQFYHEDMPLMSSSTPS 521
DB 1171 VTLTVH-----TTPTINAENQKIALQNDQIVLRCAPAKALPPVRLWTY-EGEKIDSQILPH 1226
QY 522 VGRVSPSFLITE-----CHSGNYYCTADNFGFQPSRSEVSLFVTPV-SRPILTLRVPRAQA 577
DB 1227 TIREGALVQNVKLENTGVFVQVNSLAGED-----SLSYLTIVHEKPIISEVPGVD 1281
QY 578 VV-GDLELHCAPRGPSPILYWFYHEDVTLGSSSAPSGGEASFNL-----SLTAE 627
DB 1282 VVKGFTIEIPCA-TGVPEVIRTNKNGIDLKMD-----EKKFSVDNLTIRIYEADKN 1334
QY 628 HSGNYS-----RANGLVAHQSDTISLSVTPVSRPILTFRAPRAQAVVGDLLLELHCEAL 683
DB 1335 DIGNINCVVTNEAGTSQMTHTVDVQPPILFSTQNTT-----AVVGDRELKCYV 1386
QY 684 RGSSPILYWFYHEDVTLG---KISAPSGGGSFNLSLATTGHSIGVSCAADNGL-EAQRSE 739

DB 1387 EASPPASVTWFRGIALGTDTKGYVWESDGLTVLQSASVEDATIVTCKASNPAGKAEANL 1446
QY 740 WYTLKVAGEWALPTSSSTSEN 759
DB 1447 QVTVIASPDIKDPDVVTQES 1466

RESULT 14
T42633
connectin/titin - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42633
R:Yajima, H.; Ohtsuka, H.; Kawamura, Y.; Kume, H.; Murayama, T.; Abe, H.; Kimura, S.; Ma
Biochem. Biophys. Res. Commun. 223, 160-164, 1996
A:Title: A 11.5-kb 5'-terminal cDNA sequence of chicken breast muscle connectin/titin re
A:Reference number: Z22221; MUID:96254045; PMID:8660363
A:Accession: T42633
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-4162 <YAJ>
A:Cross-references: UNIPROT:Q98918; EMBL:D83390; NID:g1513029; PIDN:BA11908.1; PID:g1513
A:Experimental source: breast muscle
C:Keywords: skeletal muscle

Query Match 7.5%; Score 297.5; DB 2; Length 4162;
Best Local Similarity 23.2%; Pred. No. 1.1e-10;
Matches 200; Conservative 113; Mismatches 327; Indels 221; Gaps 51;

QY 5 VILIYLAIVSQGPARTPRPIIFLOPPWTTVFGGERVLTCKGFRFYS-----PQ-KTKWY 58
DB 2956 VLYVNAF-----EPPQIIQELQF--TTVESG-----KPARFCALISGKPPQKWSY 3000
QY 59 --HRYLKG---EILRETPDNILEV-----QESGEYRCAQSGSPSSPVHLDP-----SSA 103
DB 3001 KDDQQLSPGFCKFLHDAQEYTLILLIETFPEDSAVYTCEAKN-----DYGVAITSA 3051
QY 104 SLILQAPLSV-----FEGDSVVLRCRAKAEVTLNNTIYKNDV 141
DB 3052 SLSVEIPEVSPLEVPYPAVIVPLRDATVSEGSARFQCRVTG-TDLKVSWSKORE 3110
QY 142 L--AFLNKRTRDF-----HIPHACLKONGARCTGYKESCCPVSNSNTVKIQVEPFF---- 189
DB 3111 IKPSRFRMTQFEDTYQLEIAEAYPEDEGTVTFVNASVGVQVSTAILKLEAPEKIMYEK 3170
QY 190 -----TRPVLRASSFQPIIS--GNPVLTCETQLSLERSDVLPRFRFRDDQTL- 235
DB 3171 LEEETEMEVKVAPILR-RLRLEPLEVAVNHVAKFTCEVETPN-----VKFOMYKAGREY 3224
QY 236 -GLGWSL--SPNF---QITAMWSKDSGFYCKAATMPSHVSIDSPSRWIQVQIPASHPVL 289
DB 3225 DDKYSIRSSNVLTLEIPRQVVDCCGYSCASQNHGCV---SSTAFLTVTEP----- 3275
QY 290 TLSPEKALNFEGTKVTLHCETQEDSLR-----TLRYFVHEGVPLRHKSVRCERGAS 340
DB 3276 ---PRFIKLDSRLV---KQHDSTRYCKVGGSPKIKVTWYKGETEIHPSK-----YS 3324
QY 341 ISF-----SLTTNSGNYYCTADNGLGAKPSKAVSLSVTPVS-----HPVLNLS 385
DB 3325 MSFVDSVAVLEMHNLISVEDSDGYSCEAQNPAGS-ASTSTSLKVKAPPFTKPPHVPQTL- 3382
QY 386 SPEDLIFEGAKVTLHCEAQROSLPILYQFYHEDDAALER-----RSANSAGVAISFSIT 439
DB 3383 -----KGSVDHLECELO-GTTPPQISWYKDKREIRSSKKYKVMSENVLASIHILNVD 3434
QY 440 AEHSGNYYCTADNFGFQPSRKAVALSITVPVSHVPLTSSAALTFEGATVTLHCEVQBG 499
DB 3435 AD-VGEYHCKAVNDVGSD--SCIGSVTLRAP---PTFVKKLSDVTVVVGETIELQAAVEGA 3489
QY 500 SP-QILY-----QFYHEDMPLMSSSTPSVGRVSPFSFLTEGHSIGNYYCTADNFGFQPSR 553
DB 3490 QPISVLWLKDKGEIITRESENLMISYSENVALSKIG-NAEPTNAGKYICOIKNDAGFQ--- 3545

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 11:23:49 ; Search time 102.374 Seconds
(without alignments)
3796.562 Million cell updates/sec

Title: US-09-724-254A-44
Perfect score: 3993
Sequence: 1 MLLWVILLVAPVSGQFART.....MVLKVGAWALPTSSTSEN 759

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3922	98.2	977	2 Q96RD9	Q96rd9 homo sapien
2	1417.5	35.5	734	2 Q96LA4	Q96la4 homo sapien
3	1417.5	35.5	734	2 Q96P31	Q96p31 homo sapien
4	1417.5	35.5	742	2 Q8N6S2	Q8n6s2 homo sapien
5	1407.5	35.2	740	2 Q96P29	Q96p29 homo sapien
6	1064	26.6	639	2 Q96P30	Q96p30 homo sapien
7	954	23.9	437	2 Q8NF56	Q8nf56 homo sapien
8	927.5	23.2	582	2 Q8OWN2	Q8own2 mus musculus
9	927.5	23.2	595	2 Q68SN8	Q68sn8 mus musculus
10	868.5	21.8	508	2 Q96LA5	Q96la5 homo sapien
11	826.5	20.7	515	2 Q96PJ5	Q96pj5 homo sapien
12	820.5	20.5	515	2 Q96RE0	Q96re0 homo sapien
13	772	19.3	360	2 Q8N732	Q8n732 homo sapien
14	692.5	17.3	508	2 Q8BJA5	Q8bjas mus musculus
15	647	16.2	509	2 Q91VK7	Q91vk7 mus musculus
16	641	16.1	509	2 Q96YJ5	Q96yj5 m mman-g pr
17	639	16.0	428	2 Q96PJ6	Q96pj6 homo sapien
18	639	16.0	429	2 Q96LA6	Q96la6 homo sapien
19	628	15.7	366	2 Q8N759	Q8n759 homo sapien
20	548	13.7	124	2 Q6UY46	Q6uy46 homo sapien
21	543.5	13.6	154	2 Q8N733	Q8n733 homo sapien
22	534.5	13.4	422	2 Q96PJ3	Q96pj3 homo sapien
23	481	12.0	722	2 Q6GNB3	Q6gnb3 xenopus lae
24	448.5	11.2	426	2 Q6BAA4	Q6baa4 homo sapien
25	446.5	11.2	626	2 Q6DCH3	Q6dch3 xenopus lae
26	428.5	10.7	357	2 Q8SPW5	Q8spw5 macaca fasc
27	418.5	10.5	374	1 FCG1 HUMAN	P12314 homo sapien
28	418	10.5	300	2 Q68SP0	Q68sp0 mus musculus
29	418	10.5	324	2 Q7TWH2	Q7tmh2 mus musculus
30	418	10.5	343	2 Q8RAY0	Q8ray0 mus musculus
31	417	10.4	343	2 Q8BYS4	Q8bys4 mus musculus

32	415	10.4	208	2 Q80WN3	Q80wn3 mus musculus
33	405	10.1	255	2 Q9BZ16	Q9bz16 homo sapien
34	402.5	10.1	372	2 Q7YQJ5	Q7yqj5 canis famil
35	402.5	10.1	404	1 FCG1 MOUSE	P26151 mus musculus
36	401	10.0	144	2 Q9BZ14	Q9bz14 homo sapien
37	401	10.0	192	2 Q9BZ15	Q9bz15 homo sapien
38	396	9.9	330	2 Q8RI42	Q8ri42 mus musculus
39	369.5	9.3	4391	1 PGEM HUMAN	Q98160 homo sapien
40	369	9.2	349	2 Q9MZT0	Q9mzt0 bos taurus
41	360.5	9.0	4071	2 Q6KDZ1	Q6kds1 gallus gall
42	358.5	9.0	5636	2 Q96RW7	Q96rw7 homo sapien
43	347	8.7	7962	2 Q10465	Q10465 homo sapien
44	347	8.7	34350	2 Q8WZ42	Q8wz42 homo sapien
45	342	8.6	413	2 Q6ZNI1	Q6znl1 homo sapien

ALIGNMENTS

RESULT 1
Q96RD9 PRELIMINARY; PRT; 977 AA.
AC Q96RD9;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Fc receptor-like protein 5.
GN Name=FCRH5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396562; PubMed=11493702; DOI=10.1073/pnas.171308498;
RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;
RT "Identification of a family of Fc receptor homologs with preferential
RT B cell expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777(2001).
DR EMBL; AF197453; AAK93971.1; -
DR HSSP; P12319; 1F2Q.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 8.
DR SMART; SM00408; Igc2; 1.
DR PROSITE; P550835; IG_LIKE; 8.
KW Receptor.
SQ SEQUENCE 977 AA; 106496 MW; 24E4A027B25509E7 CRC64;

Query Match 98.2%; Score 3922; DB 2; Length 977;
Best Local Similarity 99.9%; Pred. No. 2.4e-254;
Matches 745; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MLLWVILLVAPVSGQFARTPRPIIFLQPPWTVFQGERVLTCKGFRFYSPQKTWYHR	60
DB	1	MLLWVILLVAPVSGQFARTPRPIIFLQPPWTVFQGERVLTCKGFRFYSPQKTWYHR	60
QY	61	YLKKEILRETPDNILVQESGVRCAQSPVHLDFSSASLIQAPLSVFEQDSVV	120
DB	61	YLKKEILRETPDNILVQESGVRCAQSPVHLDFSSASLIQAPLSVFEQDSVV	120
QY	121	LRCRAEAVTLNNTIYKNDVLAFLNKRDFH1PHACLKNGAYRCTGYKESCCPVSSNT	180
DB	121	LRCRAEAVTLNNTIYKNDVLAFLNKRDFH1PHACLKNGAYRCTGYKESCCPVSSNT	180
QY	181	VKIQQEPTPRVLRASSFPISGNPVTLTCTQLSLERSDVPPLRFRFRDDDTGLGWS	240
DB	181	VKIQQEPTPRVLRASSFPISGNPVTLTCTQLSLERSDVPPLRFRFRDDDTGLGWS	240
QY	241	LSPNFOITAMWSKDSGFYCKAATMPHSVISDSRPSWIQVQIPASHPVLTLSPKALNFE	300
DB	241	LSPNFOITAMWSKDSGFYCKAATMPHSVISDSRPSWIQVQIPASHPVLTLSPKALNFE	300


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DR SMART: SM00408; IGc2; 1.
DR PROSITE; PS00835; IG LIKE; 6.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.
SQ SEQUENCE 734 AA; 80855 MW; B3411B73A35BC668 CRC64;

Query Match 35.5%; Score 1417.5; DB 2; Length 734;
Best Local Similarity 41.6%; Pred. No. 1.6e-86;
Matches 318; Conservative 71; Mismatches 173; Indels 203; Gaps 10;

Qy 1 MLLWVILLVLPVSGQGFARTPRPIIFLOPPWTVFQGERVTLTKCKGRFFYSPO-KTKWYH 59
Db 1 MLLWVILLVLPVSGQGFARTPRPIIFLOPPWTVFQGERVTLTKCKGRFFYSPO-KTKWYH 59
Qy 60 RYLCKEILRETDPNILEVOESGEYRCQAQSPVHLDFFSSASLILQAPLSVFEQDSV 119
Db 60 RYLCKEILRETDPNILEVOESGEYRCQAQSPVHLDFFSSASLILQAPLSVFEQDSV 119
Qy 61 ---DEKLLKIKHDKI-QITEPGNYQCKTRGSSLSDAVHVEFSPDWLILQALHPVFEQDNV 116
Db 61 ---DEKLLKIKHDKI-QITEPGNYQCKTRGSSLSDAVHVEFSPDWLILQALHPVFEQDNV 116
Qy 120 VLRCRAKAEVTLNNTIYKNDNVLAFLNKRDFHPIHACLKNDGAYRGTGYKESC---CPV 176
Db 120 VLRCRAKAEVTLNNTIYKNDNVLAFLNKRDFHPIHACLKNDGAYRGTGYKESC---CPV 176
Qy 117 ILRCQCKDNKNTKQKVVYKDGKQLPNSVLEKITYNSVRDNRKSKYHCTAYRKFYLDIEV 176
Db 117 ILRCQCKDNKNTKQKVVYKDGKQLPNSVLEKITYNSVRDNRKSKYHCTAYRKFYLDIEV 176
Qy 177 SNTVKIQVEPEPTRVLRASSFPQISGNPVTLTCTQLSLERSDVPRLRFRFRDQTLG 236
Db 177 SNTVKIQVEPEPTRVLRASSFPQISGNPVTLTCTQLSLERSDVPRLRFRFRDQTLG 236
Qy 177 TSKPLNIOVQLFHPVLRASSFTPIEGSPMTLTCTQLSPQRPDQVQLQSLFRDQTLG 236
Db 177 TSKPLNIOVQLFHPVLRASSFTPIEGSPMTLTCTQLSPQRPDQVQLQSLFRDQTLG 236
Qy 237 LGWSLSPNFQITAMWSKDSGFYCKAATMPHSVISDSRPSWIOVQIPASHPVLTLSPEKA 296
Db 237 LGWSLSPNFQITAMWSKDSGFYCKAATMPHSVISDSRPSWIOVQIPASHPVLTLSPEKA 296
Qy 237 LGWSRSPRLQIPAMWTEDESGSYWCEVETVTHSIKESLSQIRVQ----- 281
Db 237 LGWSRSPRLQIPAMWTEDESGSYWCEVETVTHSIKESLSQIRVQ----- 281
Qy 297 LNPEGTGKTLHCETQSDSLRTLYRFYHEGVPLRHKSVCRCERGASISFSLTENSNGNYCT 356
Db 297 LNPEGTGKTLHCETQSDSLRTLYRFYHEGVPLRHKSVCRCERGASISFSLTENSNGNYCT 356
Qy 282 ----- 281
Db 282 ----- 281
Qy 357 ADNLGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHH 416
Db 357 ADNLGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHH 416
Qy 282 -----RVFVSNVNLEIRPTGGQLIEGENMVLICSAQSGSTVTFWSHK 324
Db 282 -----RVFVSNVNLEIRPTGGQLIEGENMVLICSAQSGSTVTFWSHK 324

RESULT 4
Q8N6S2
ID Q8N6S2 PRELIMINARY; PRT; 742 AA.
AC Q8N6S2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE FCRH3 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Query Match 35.5%; Score 1417.5; DB 2; Length 742;
Best Local Similarity 41.6%; Pred. No. 1.6e-86;
Matches 318; Conservative 71; Mismatches 173; Indels 203; Gaps 10;

Qy 1 MLLWVILLVLPVSGQGFARTPRPIIFLOPPWTVFQGERVTLTKCKGRFFYSPO-KTKWYH 59
Db 1 MLLWVILLVLPVSGQGFARTPRPIIFLOPPWTVFQGERVTLTKCKGRFFYSPO-KTKWYH 59
Qy 60 RYLCKEILRETDPNILEVOESGEYRCQAQSPVHLDFFSSASLILQAPLSVFEQDSV 119
Db 60 RYLCKEILRETDPNILEVOESGEYRCQAQSPVHLDFFSSASLILQAPLSVFEQDSV 119
Qy 61 ---DEKLLKIKHDKI-QITEPGNYQCKTRGSSLSDAVHVEFSPDWLILQALHPVFEQDNV 116
Db 61 ---DEKLLKIKHDKI-QITEPGNYQCKTRGSSLSDAVHVEFSPDWLILQALHPVFEQDNV 116
Qy 120 VLRCRAKAEVTLNNTIYKNDNVLAFLNKRDFHPIHACLKNDGAYRGTGYKESC---CPV 176
Db 120 VLRCRAKAEVTLNNTIYKNDNVLAFLNKRDFHPIHACLKNDGAYRGTGYKESC---CPV 176
Qy 117 ILRCQCKDNKNTKQKVVYKDGKQLPNSVLEKITYNSVRDNRKSKYHCTAYRKFYLDIEV 176
Db 117 ILRCQCKDNKNTKQKVVYKDGKQLPNSVLEKITYNSVRDNRKSKYHCTAYRKFYLDIEV 176
Qy 177 SNTVKIQVEPEPTRVLRASSFPQISGNPVTLTCTQLSLERSDVPRLRFRFRDQTLG 236
Db 177 SNTVKIQVEPEPTRVLRASSFPQISGNPVTLTCTQLSLERSDVPRLRFRFRDQTLG 236
Qy 177 TSKPLNIOVQLFHPVLRASSFTPIEGSPMTLTCTQLSPQRPDQVQLQSLFRDQTLG 236
Db 177 TSKPLNIOVQLFHPVLRASSFTPIEGSPMTLTCTQLSPQRPDQVQLQSLFRDQTLG 236
Qy 237 LGWSLSPNFQITAMWSKDSGFYCKAATMPHSVISDSRPSWIOVQIPASHPVLTLSPEKA 296
Db 237 LGWSLSPNFQITAMWSKDSGFYCKAATMPHSVISDSRPSWIOVQIPASHPVLTLSPEKA 296
Qy 237 LGWSRSPRLQIPAMWTEDESGSYWCEVETVTHSIKESLSQIRVQ----- 281
Db 237 LGWSRSPRLQIPAMWTEDESGSYWCEVETVTHSIKESLSQIRVQ----- 281
Qy 297 LNPEGTGKTLHCETQSDSLRTLYRFYHEGVPLRHKSVCRCERGASISFSLTENSNGNYCT 356
Db 297 LNPEGTGKTLHCETQSDSLRTLYRFYHEGVPLRHKSVCRCERGASISFSLTENSNGNYCT 356
Qy 282 ----- 281
Db 282 ----- 281
Qy 357 ADNLGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHH 416
Db 357 ADNLGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQFHH 416
Qy 282 -----RVFVSNVNLEIRPTGGQLIEGENMVLICSAQSGSTVTFWSHK 324
Db 282 -----RVFVSNVNLEIRPTGGQLIEGENMVLICSAQSGSTVTFWSHK 324
Qy 417 ED--AALERSANSAGGVAISFLTAESHGNYCYCTADNGFGPQRKAVSLSIITVPVSHV 474
Db 417 ED--AALERSANSAGGVAISFLTAESHGNYCYCTADNGFGPQRKAVSLSIITVPVSHV 474
Qy 325 EGRVSLGRKT-----QRSLLAELH-----V 345
Db 325 EGRVSLGRKT-----QRSLLAELH-----V 345
Qy 475 LTLSSAEALTFEGATVTLHCEVORGSPQILYQFVHEDMPLWSSSTPSVGRVSFSLTEG 534
Db 475 LTLSSAEALTFEGATVTLHCEVORGSPQILYQFVHEDMPLWSSSTPSVGRVSFSLTEG 534
Qy 346 LTLKESDA----- 353
Db 346 LTLKESDA----- 353
Qy 535 HSGNYCTADNGFGPQRSEVVSFLVTVVPSRPILTLVPRQAQAVGDLLEHCEAPRGSP 594
Db 535 HSGNYCTADNGFGPQRSEVVSFLVTVVPSRPILTLVPRQAQAVGDLLEHCEAPRGSP 594
Qy 354 --GRYCAADNVHSPILSTWIRTVLPVSHPVLTFRAPRAHTVVDLLEHCESLRGSP 411
Db 354 --GRYCAADNVHSPILSTWIRTVLPVSHPVLTFRAPRAHTVVDLLEHCESLRGSP 411
Qy 595 PILYFWYHEDVTLGSSAPSGGASFNLSLTAEHSGNYSCAANGLVAQHSDTISLVIV 654
Db 595 PILYFWYHEDVTLGSSAPSGGASFNLSLTAEHSGNYSCAANGLVAQHSDTISLVIV 654
Qy 412 PILYFWYHEDVTLGSSAPSGGASFNLSLTAEHSGNYSCAANGLVAQHSDTISLVIV 471
Db 412 PILYFWYHEDVTLGSSAPSGGASFNLSLTAEHSGNYSCAANGLVAQHSDTISLVIV 471
Qy 655 PVSRPILTFAPRAQAVGDLLEHCEALRGSPPIYFWYHEDVTLGKISAPSGGASFN 714
Db 655 PVSRPILTFAPRAQAVGDLLEHCEALRGSPPIYFWYHEDVTLGKISAPSGGASFN 714
Qy 472 PVSRPILTFAPRAQAVGDLLEHCEALRGSPPIYFWYHEDVTLGKISAPSGGASFN 531
Db 472 PVSRPILTFAPRAQAVGDLLEHCEALRGSPPIYFWYHEDVTLGKISAPSGGASFN 531
Qy 715 LSLTTHSGNYSCAANGLVAQHSMTVLAQVGEWALPTSSTSEN 759
Db 715 LSLTTHSGNYSCAANGLVAQHSMTVLAQVGEWALPTSSTSEN 759
Qy 532 LSLTTHSGNYSCAANGLVAQHSMTVLAQVGEWALPTSSTSEN 568
Db 532 LSLTTHSGNYSCAANGLVAQHSMTVLAQVGEWALPTSSTSEN 568
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QY 417 ED--AALRRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSIITVPVSHPV 474
DB 325 EGRVRSLGKRT-----ORSLLAELH-----V 345
QY 475 LTLSSAALTFEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPVGVSFSLTEG 534
DB 346 LTVKESDA-----V 353
QY 535 HSGNYCTADNGFGPQRSSEVSLFVTPVPSRPILTLRVPRQAQVVGDLLELHCEAPRGSP 594
DB 354 --GRYYCAADNVHSPILSTWIRVTPVSHPVLTFRAPRAHTVVGDLLELHCESLRGSP 411
QY 595 PLYFYHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCANNGLVAOHSDTISLSVIV 654
DB 412 PLYFYHEDVTLGNSAPSGGASFNLSLTAHSGNYSCADNGLGAQHSGLRVTV 471
QY 655 PVSRRPILTFRAPRAQVVGDLLELHCEALRGSSPILYFYHEDVTLGKISAPSGGASFN 714
DB 472 PVSRRPILTLRAPGAQVVGDLLELHCESLRGSPILYFYHEDVTLGNSAHSAGGASFN 531
QY 715 LSLTTEHSGIYCEADNGLAQRSEMVTILKVAGEWALPTSSTSEN 759
DB 532 LSLTTEHSGNYSCADNGLGAQHSKVTLNVGT-----TSRN 568
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RESULT 5

```
Q96P29 ID Q96P29 PRELIMINARY; PRT; 740 AA.
AC Q96P29;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE SH2 domain-containing phosphatase anchor protein 2c.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu M.-J., Zhao R., Zhao Z.J.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF416903; AAL13292.1; --
DR HSSP; P12319; 1F2Q.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00408; Igc2; 1.
DR PROSITE; PS50835; IG_LIKE; 6.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.
SQ SEQUENCE 740 AA; 81440 MW; 038AFA83A2909E46 CRC64;
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Query Match 35.2%; Score 1407.5; DB 2; Length 740;
Best Local Similarity 41.4%; Pred. No. 7.5e-86;
Matches 319; Conservative 71; Mismatches 172; Indels 209; Gaps 11;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLPQPTWTFQGERVTLTKCFRFSYQ-KTKVNH 59
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLPQPTWTFQGERVTLTKCFRFSYQ-KTKVNH 60
QY 60 RYLKGEILRETPDNLVEQSGEYRCQAGSPSLSPVHLDFSSASLILQAPLSVFEQDSV 119
DB 61 ---DEKLLIKKDKI-QITEPGNYQCKTRGSSLSDAVHFSPDWLILQALHPVFGDNV 116
QY 120 VLFRCRAEAVTLNNTIYKNDVLAFLNKRDTFHI PHACLKDNKAYRCTGYKSC---CPV 176
DB 117 ILRCQCKDNKNTQKVVYKDGKQLPNSYLEKITVNSVSRDNSKYHCTAYRKFIYLDIEV 176
QY 177 SNTVIVQVEPTRTVLRASSQPISGNPVTLTCTQLSLERSDYLFRFRDDDTLG 236
DB 177 TSKPLNIQVQELFLHPVLRASSSTPIEGSPMTLTCTQLSPQDVLQFSLFRDQTLG 236
QY 237 LGWSLSPNFQITAMWKSDFYCKAATWPHSVISDSPRSWIQVQIPASHVPLTILSPEKA 296
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DB 237 LGWSRSLQIPAMWTEDSGSYNCEVETVTHSIKRSIRSQIRVQ----- 281
QY 297 INFEGTKVTLHCETQEDSLTLIRFYHEGVPLRHSVRCERGASISFSLTENSNGYCT 356
DB 282 ----- 281
QY 357 ADNGLGAKPSKAVSLSVTPVSHPVNLNSPEDLIFEGAKVTLHCEAQRGSLPILYQFHH 416
DB 282 -----RVPSNVNLEIRPTGGQLIEGENWVLICSVAGSGTTFSSHK 324
QY 417 ED--AALERSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSIITVPVSHPV 474
DB 325 EGRVRSLGKRT-----ORSLLAELH-----V 345
QY 475 LTLSSAALTFEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPVGVSFSLTEG 534
DB 346 LTVKESDA----- 353
QY 535 HSGNYCTADNGFGPQRSSEVSLFV-----TVPVSRPILTLRVPRQAQVVGDLLELHCE 588
DB 354 --GRYYCAADNVHSPILSTWIRVTPVSHPVLTFRAPRAHTVVGDLLELHCE 411
QY 589 APRGSPILYFYHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCANNGLVAOHSDTI 648
DB 412 SLRGSPILYFYHEDVTLGNSAPSGGASFNLSLTAHSGNYSCADNGLGAQHSGLV 471
QY 649 SLSVIVPVSRRPILTFRAPRAQVVGDLLELHCEALRGSSPILYFYHEDVTLGKISAPSG 708
DB 472 SLRVTPVPSRRPILTLRAPGAQVVGDLLELHCESLRGSPILYFYHEDVTLGNSAHS 531
QY 709 GGASFNLSLTTTEHSGIYCEADNGLAQRSEMVTILKVAGEWALPTSSTSEN 759
DB 532 GGASFNLSLTTTEHSGNYSCADNGLGAQHSKVTLNVGT-----TSRN 574

RESULT 6
Q96P30 ID Q96P30 PRELIMINARY; PRT; 639 AA.
AC Q96P30;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE SH2 domain-containing phosphatase anchor protein 2b.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu M.-J., Zhao R., Zhao Z.J.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF416902; AAL13291.1; --
DR HSSP; P12319; 1F2Q.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; Igc2; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.
SQ SEQUENCE 639 AA; 69928 MW; DEAD7AD4E64CA984 CRC64;
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Query Match 26.6%; Score 1064; DB 2; Length 639;
Best Local Similarity 34.0%; Pred. No. 6.8e-63;
Matches 259; Conservative 62; Mismatches 149; Indels 292; Gaps 11;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLPQPTWTFQGERVTLTKCFRFSYQ-KTKVNH 59
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLPQPTWTFQGERVTLTKCFRFSYQ-KTKVNH 60
QY 60 RYLKGEILRETPDNLVEQSGEYRCQAGSPSLSPVHLDFSSASLILQAPLSVFEQDSV 119
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Db 61 ---DEKLLKIKHKDKI-QITEPGNYQCKTRGSSLSDAVHVFEFSPDWLILQALHPVFEQDNV 116
Qy 120 VLRCAKAEVTLNNTIYKNDNLAFNLKTRDFHPIHACLKNDGAYRCTGYKESCCPVSSN 179
Db 117 ILRCQKDNKNTQKQVYKDGKQLPNSYNLEKITEVNSRDNKSYCHCTAYRK-----168
Qy 180 TVKIQVQEPTRPVLRASSFPQISGNPVUTCTQLSLERSDVLPRFRPRDRDQTLGLGW 239
Db 169 -----168
Qy 240 SLSPNFQITAMWSKDSGFYCKAATMHPHSVISDSPRSWIOVQIPASHPVLTLSPKALNF 299
Db 169 -----FY-----ILDI 174
Qy 300 EGTKVTLHCFTQBSLRLTYRFYHEGVPLRHKSVCRCERGASISFSLTTENSNGNYCTADN 359
Db 175 EVTSKPLNIQVQ-----186
Qy 360 GLAKPSKAVSLSVTPVSHVPLNLSPEDLIFEGAKVTLHCEAQRGSLPILYQFHED- 418
Db 187 -----GVPVSNVNLEIRPTGGQLIEGENMVLICSAQCGSGTTFVSWHKEGR 232
Qy 419 -AALERRSANSAGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSIITVPVSHPVLT 477
Db 233 VRSIGRKT-----QRSLLAEHL-----VLTV 253
Qy 478 SSAEALTFFEGATVTLHCEVQSGSPQILYQFYHEDMPLMSSSTPSVGRVSFSLTEGHS 537
Db 254 KESDA-----G 259
Qy 538 NYCTADNGFGPORSSEVSLFVTPVSRPILTRVPRQAQVVGDLLELHCEAPRGSPPI 597
Db 260 RYCAADNVHSPILSTWIRTVIRPVSHPVLTFRAPRAHTVVGDLLELHCESLRSGSPPI 319
Qy 598 YWFYHEDVTLGSSAPSGGASFNLSLTAHSGNYCEANNGVLAQHSOTISLSIVPVVS 657
Db 320 YRTHEDVTLGNSAPSGGASFNLSLTAHSGNYSCDADNGAGAHQSHGVSRVTPVVS 379
Qy 658 RPLTFRAPRAQAVVGDLLELHCEALRGSSPILYFVYHEDVTLGKISAPSGGASFNLS 717
Db 380 RPLVTLRAPCAQAVVGDLLELHCESLRGSSPILYFVYHEDVTLGNSAHSGGASFNLS 439
Qy 718 TTHSGIYSCDANGLEAQRSEMVTLKVAQEWALPTSSISEN 759
Db 440 TTHSGIYSCDANGLEAQRSEMVTLKVAQEWALPTSSISEN 759
Db 440 TTHSGIYSCDANGLEAQRSEMVTLKVAQEWALPTSSISEN 759

RESULT 7
Q8NF56
ID Q8NF56 PRELIMINARY; PRT; 437 AA.
AC Q8NF56;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE FLJ00333 protein (fragment).
GN Name=FLJ00333;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK090423; BAC03404.1; -
DR InterPro; IPR003599; Ig.
DR PFam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 3.
DR PROSITE; PS50835; IG_LIKE; 3.
FT NON_TER 1
SQ SEQUENCE 437 AA; 46521 MW; F56DED36523E52CA CRC64;

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Query Match 23.9%; Score 954; DB 2; Length 437;
Best Local Similarity 67.2%; Pred. No. 9.7e-56;
Matches 199; Conservative 17; Mismatches 64; Indels 16; Gaps 4;

Qy 464 LSITVPVSHVPLTSSAEALT-----FEGA-----TVTLHCEVQSGSPQILYQFHED 511
Db 8 LKIHVSLTH---FLSQFQCLAPSPSPGPFQAQVVGDLLELHCEAPRGSPPIYWFYHED 64
Qy 512 MPLWSSSTPSVGRVSFSLTEGHSGNYCTADNGFGPORSSEVSLFVTPVSRPILTLR 571
Db 65 VTLCSSASGSGEASFNLSLTAHSGNYSCDANGVLAQHSOTISLSIVPVSRPILTLR 124
Qy 572 VPRQAQVVGDLLELHCEAPRGSPPIYFVYHEDVTLGSSAPSGGASFNLSLTAHSGN 631
Db 125 APRQAQVVGDLLELHCEALRGSSPILYFVYHEDVTLGKISAPSGGASFNLSLTTESGI 184
Qy 632 YSCDANGVLAQHSOTISLSIVPVSRPILTRAPRAQAVVGDLLELHCEALRGSSPILY 691
Db 185 YSCDANGVLAQHSOTISLSIVPVSRPILTRAPGTHAAVVGDLLELHCEALRGSPILY 244
Qy 692 WYFVHEDVTLGKISAPSGGASFNLSLTTBHSIYSCDANGVLAQHSOTISLSIVPVSR 747
Db 245 RFPHEDVTLGNSRSPS-GGASLNLSLTAHSGNYSCDANGVLAQHSOTISLITG 299

RESULT 8
Q80WN2
ID Q80WN2 PRELIMINARY; PRT; 582 AA.
AC Q80WN2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE EXMAS1-like protein 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Nakayama Y., Maher S.B., Weissman S.M., Bothwell A.L.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY158090; AAC020873.1; -
DR HSSP; P12319; 1F20.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG_LIKE; 5.
SQ SEQUENCE 582 AA; 65248 MW; 44321E93FB9EDF06 CRC64;

Query Match 23.2%; Score 927.5; DB 2; Length 582;
Best Local Similarity 41.9%; Pred. No. 8.5e-54;
Matches 209; Conservative 82; Mismatches 161; Indels 47; Gaps 9;

Qy 3 LWVILLVLPVSGQFARTPRPIIFLPPWTVFQGRVTLTKGFRFYSQPKTKWYHYL 62
Db 1 MWLTLVTVFVNGQHEAAQSVSVLQPPWTVFQGRVTLTKGFRFYSQPKTKWYHYL 58
Qy 63 GKEILRETDP-----NILEVQESGYRCOAQSGPLSSPVHLDFFSASLILQAPLSVFEG 116
Db 59 -RKTQKTPGALVIRKATLKVHESGYWCQADSLPLSMHVNFESDFVLQAPPAVFE 117
Qy 117 DSVILRCRAKAEVTLNN-TIYKNDNVLAFLNKRTPHPIHACLKNDGAYRCTGYKESCC 173
Db 118 DSVILRCYAKKGIETATLTFYKDGKALT-LHQSELSIHHANLKONGQYKCTSKKWSFG 176
Qy 174 CPVSSNTVKIQVQEPTRPVLRASSFPQISGNPVUTCTQLSLERSDVLPRFRPRDRDQ 233
Db 177 SLYTSNTVGVQVQELFPFRVLRARSHPIDGSPVTLTCTQLSAQKSDARLQCFERNLQ 236
Qy 234 TLGLGWSLSPNFQITAMWSKDSGFYCKAATMHPHSVISDSPRSWIOVQIPASHPVLTLSP 293

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Db 237 LLGSCSSSEPHIPAIWTEESRRYQCKAETVNSQVRKQSTAFIIPVQASARFQTHIP 296
QY 294 EKALNFEKTKVTLHCETQEDSLTLRYFHEGVP-----LRHKSVCRCGASIS 342
Db 297 ASKLVEFGQLLLNCV-----KGVPGLKFSWYKMDLNEETKILKSSNAE 343
QY 343 FSLITTEN---SGNYCTADNGLGAKPSKAVLSVTPVSHVPLNLSPPEDLIFECAKVTL 399
Db 344 FKISQVNSIDAGEYHCEATNSRRSFVSRAPFTIKVPVSQPVLTJSTGKTQALEGLMTL 403
QY 400 HCEAQRGSLPILYQFHEDDALERRSANSAGGVAISFSLTAHSGNYYCTADNGLGPGPORS 459
Db 404 HCQSQRGSPCLLYEPFYENVSLGNSILSGGAYFNFSMSTERSGNYCYCTADNGLGAQCS 463
QY 460 KAVLSLSI-----TVPVS 471
Db 464 EAIRISIFDMTKNRSVPM 482

RESULT 9
Q68SN8
ID Q68SN8 PRELIMINARY; PRT; 595 AA.
AC Q68SN8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Fc receptor-like protein 3.
GN Name=Fch3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Spleen;
RX PubMed=15302849;
RA Davis R.S., Stephan R.P., Chen C.C., Dennis G. Jr., Cooper M.D.;
RT "Differential B cell expression of mouse Fc receptor homologs.";
RL Int. Immunol. 16:1343-1353(2004).
DR EMBL; AY506558; AAS91578.1; -.
DR GO; GO:0004872; Fc receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; Ig; 5.
DR SMART; SM00408; IgC2; 4.
DR PROSITE; PS50835; IG_LIKE; 5.
KW Receptor.
SQ SEQUENCE 595 AA; 66619 MW; 6AEEDB8E2F6AFACF CRC64;

Query Match
Best Local Similarity 23.2%; Score 927.5; DB 2; Length 595;
Matches 209; Conservative 82; Mismatches 161; Indels 47; Gaps 9;

QY 3 LWVILLVLPVSGQFARTPRPIIFLOPPWTTVFGERVTLTCGFRFSPQKTKWYHRYL 62
Db 14 MWLTLLVTPVNGQHEAAQSVSLQPPWTFRGEVTLTCYRFGFSVPQTKWYQK-- 71
QY 63 GKEILRETPD-----NILEVQESGEYRCQAGSPLSPVHLDFSSASLILOAPLSVPEG 116
Db 72 -RKTVPQTPGALVIAKHTLVKVESGEYWCQADSLSPSMHVNVEFSEDFVLQAPPVAFEG 130
QY 117 DSVLRCRAKABVTLNN--TIYKNDVLAFLNKRDTDFHLPACLKNDGAYRCTGVKESC-- 173
Db 131 DSVLRCYAKKGIETITFYKDGKALT-LHQSELSIHHANLKDNGQYKCTSKKKKWSFG 189
QY 174 CPVSSNTVKIQVEPFRPVLRASSFPQISGNPVTLCITQLSLERSDVPLRFRFRDDQ 233
Db 190 SLYTSNTVGVQVQELFPRPVLRAEHPIDGSPVTLTCQTLQSAQSDARLQCFERNLQ 249
QY 234 TLGLGWSLSPNFQITAMWSKDSGFWCKAAATPHSVISDSRSPWIQVQIPASHPVLTLSP 293
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Db 250 LLGSCSSSEPHIPAIWTEESRRYQCKAETVNSQVRKQSTAFIIPVQASARFQTHIP 309
QY 294 EKALNFEKTKVTLHCETQEDSLTLRYFHEGVP-----LRHKSVCRCGASIS 342
Db 310 ASKLVEFGQLLLNCV-----KGVPGLKFSWYKMDLNEETKILKSSNAE 356
QY 343 FSLITTEN---SGNYCTADNGLGAKPSKAVLSVTPVSHVPLNLSPPEDLIFECAKVTL 399
Db 357 FKISQVNSIDAGEYHCEATNSRRSFVSRAPFTIKVPVSQPVLTJSTGKTQALEGLMTL 416
QY 400 HCEAQRGSLPILYQFHEDDALERRSANSAGGVAISFSLTAHSGNYYCTADNGLGPGPORS 459
Db 417 HCQSQRGSPCLLYEPFYENVSLGNSILSGGAYFNFSMSTERSGNYCYCTADNGLGAQCS 476
QY 460 KAVLSLSI-----TVPVS 471
Db 477 EAIRISIFDMTKNRSVPM 495

RESULT 10
Q96LA5
ID Q96LA5 PRELIMINARY; PRT; 508 AA.
AC Q96LA5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fc receptor-like protein 2 (FCRH2).
GN Name=FCRH2; ORFNames=UNQ9236;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396562; PubMed=11493702; DOI=10.1073/pnas.171308498;
RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;
RT "Identification of a family of Fc receptor homologs with preferential B cell expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=2287296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY043465; AAQ91778.1; -.
DR EMBL; AY358130; AAQ88497.1; -.
DR HSP; P12319; IF2Q.
DR Genew; HGNC:14875; SPAP1.
DR GO; GO:0004872; Fc receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 3.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Receptor.
SQ SEQUENCE 508 AA; 55541 MW; 9AB30E0411B41EDC CRC64;

Query Match
Best Local Similarity 21.8%; Score 868.5; DB 2; Length 508;
Matches 220; Conservative 60; Mismatches 134; Indels 211; Gaps 12;

QY 104 SLILOAPLSVPEGSDVLCRAKAEVTLNNTYKNDN-VLAFLNKRDTDFHLPACLKNDG 162
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Db 19 SLTLVAPSSVFEKDSIVLKCQGEONWKIQMAYHKONKELSVFKPSDFLIQSAVLSDSG 78
Qy 163 AYRC-TGYKESCCPVSSNTVKIQVEPFTPLVRASSQFISGNPVTLTCTETQLSLERSD 221
Db 79 NYFCSTKGQLFLWDKTSNI VKIQVELFQRPVLTASSQFIEGGPVSLKCETRLSPQLD 138
Qy 222 VPLRFRFRDDQTLGLGWSLSPNFOITAMWSKDSGFYWCXAAATMPSHVISDSRPSHIQVQ 281
Db 139 VOIQCFPFRENOVLGSGWSSSPLOISAVMSDSTGYSWYCAETVTHIRKQSLQSQIHVQ 198
Qy 282 IPASHPVLTLSPEKALNFEGTKVTLHCETQEDSLRTLYRYFHEGVPLRHKSVCERGASI 341
Db 199 ----- 198
Qy 342 SFSLTTESSNGYYCTADNGLGAKPSKAVSLVTPVPSHPVLNLSPPEDLIFEGAKVTLHC 401
Db 199 -----RIPISNVLSLEIRAFGGQVTEQKLLILC 226
Qy 402 EAORGSLPILYQPHHEDALERRANSAGVA-ISFSLTAHSGNYYCTADNFGFGPQSRK 460
Db 227 SV-----AGGTGNVTFSWYREATG-----TSMGKKTOR 254
Qy 461 AVLSITVPVSHPVLTLSAEALTFFGATVTLHCEVQSGPQILYQFYHEDMPLMSSSTP 520
Db 255 SLSAELEIP----- 263
Qy 521 SVGRVSFSLSLTCBHSNGYYCTADNFGFGPQSRVSLFVTPVPSRPTILTRVPRAQAVG 580
Db 264 -----AVKESDAGKYCYRADNHVPQSKVNI PVIRPVSRPVLTLSRPGAQAVG 314
Qy 581 DLLELHCEAPRGSPPILYFYHEDVTLGSSASPSGSGEASFNLSLTAHSGNYYSCAANGL 640
Db 315 DLLELHCEALRGSPPILYQFYHEDVTLGNSAPSPPGSGASFNLSLTAHSGNYYSCAANGL 374
Qy 641 VAQHSITISLVIVP--VSPILTRAPRAQAVGDLLELHCEALRGSSPILYFYHEDV 698
Db 375 GAQCSAVPVISGPGYRDLMT--AGVLWGLFGLV-----GFTGVALLLYALFHF-- 423
Qy 699 TLGKISAPSGGASFNLSLTFHSG 723
Db 424 ---KISGES-----SATNEPG 437
Qy 966PJ5
ID Q96PJ5 PRELIMINARY; PRT; 515 AA.
AC Q96PJ5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE IFGP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tonsil;
RX MEDLINE=22033006; PubMed=12037601; DOI=10.1007/s00251-002-0436-x;
RA Guseinikov S.V., Ershova S.A., Mechetina L.V., Najakshin A.M.,
RA Volkova O.Y., Alabyev B.Y., Taranin A.V.;
RT "A family of highly diverse human and mouse genes structurally links
RT leukocyte FCg, gp42 and PECAM-1.";
RL Immunogenetics 54:87-95(2002).
DR EMBL; AF329490; AAL23900.1; -.
DR HSSP; P12319; IF2Q.
DR InterPro; IPR007110; Ig-like.
DR SMART; PF00047; Ig; 3.
DR PROSITE; PS50835; IG_LIKE; 4.
SQ SEQUENCE 515 AA; 57224 MW; F3B7AD14FB1B449A CRC64;
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Query Match 20.7%; Score 826.5; DB 2; Length 515;
Best Local Similarity 43.5%; Pred. No. 4.3e-47;
Matches 184; Conservative 55; Mismatches 161; Indels 23; Gaps 6;

Qy 1 MLLWVILLVLPVSGQFARTPRPIIFLOQPWTTVFOGERVTLTCKGRFYSPQTKWYHR 60
Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOQPWTTVFOGERVTLTCKGRFYSPQTKWYHR 60
Qy 61 YLCKEILRETPDNLIVQESGEYRCQAQSGSLSSPVHLDFSSASLILQAPLSVFEKDSV 120
Db 61 HWGEKLTLPNGTLEVRSGLYRCQARGSPRNVPVLLFSSDSLILQAPSVFEGDTLV 120
Qy 121 LRCRAKAEVTLNNTIYK-NDNLVAFLNKRTDFH PHACLKDNKAYRCTGYKESCCPVSSN 179
Db 121 LRCHRRRKEKLTAVKYTWNGNLSISNGWDLIPQASSNNNGYRCIGYGDENDVPRSN 180
Qy 180 TVKIQVQEPFTRPVLRASSFOISGNPVTLTCTETQLSLERSDVLPRFRFRDDQTLGLG 239
Db 181 FKIKITQELFPHPELKATDSQPTGNSVNLSCETQLPPERSDTPLFHNFRRDGEVILSD 240
Qy 240 SLSPNFQITAMWSKDSGFYWCXAAATMPSHVISDSRPSHIQVQ-IPASHPVLTLSPEKALN 298
Db 241 STYPELQLPTVWRENSGSWCGAETVRGNIHKHSPSLQIHVQRI PVSGVLTETQPSGQA 300
Qy 299 FEGTKVTLHCETQEDSLRTLYRYFHEGV--PLRHKSVCERGASISFSLTTESSNGYYCT 356
Db 301 VEGEMLVLCVSAEAGTDTTFSWHREDMQESLGRKTQSLRAELPELPAIRQSHAGGYCT 360
Qy 357 ANGLGAKSKAVSLVTPVSHPVLTLSPPEDLIFEGA-----KVTLHCEAQ 404
Db 361 ADNSYG--PVQSNVLNVTVRETP-----GNRDGLVAAGATGGLLSALLAVALLFHCWRR 413
Qy 405 RGS 407
Db 414 RKS 416

RESULT 12
Q96RE0
ID Q96RE0 PRELIMINARY; PRT; 515 AA.
AC Q96RE0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fc receptor-like protein 4.
GN Name=FCRH4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396562; PubMed=11493702; DOI=10.1073/pnas.171308498;
RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;
RT "Identification of a family of Fc receptor homologs with preferential
RT B cell expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777(2001).
DR EMBL; AF397452; AAK93970.1; -.
DR HSSP; P12319; IF2Q.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
KW Receptor.
SQ SEQUENCE 515 AA; 57250 MW; 32FBD6FAB2B19D3D CRC64;

Query Match 20.5%; Score 820.5; DB 2; Length 515;
Best Local Similarity 43.3%; Pred. No. 1.1e-46;
Matches 183; Conservative 55; Mismatches 162; Indels 23; Gaps 6;

Qy 1 MLLWVILLVLPVSGQFARTPRPIIFLOQPWTTVFOGERVTLTCKGRFYSPQTKWYHR 60
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Db 1 MLLWASLAPVCGSAAAHKPVISVHPPTWTFKGERVILTCNGQFYATEKTTWYHR 60
QY 61 YLGEILRETPDNILEVQESGEYRCQAQSGPLSPVHLDPSSASLILQAPLSVFEQDSVV 120
Db 61 HYWGEKLTLPNGNTLEVRSGLYRCQAQSGPRSPVRLFFSSDSLILQAPYSVFEQDTLV 120
QY 121 LRCRAAEVTLNNTIYK-NDNVLAFLNKRDTDFHPIHACLDKNGAYRCTGYKESCCPVSN 179
Db 121 LRCHRRKEKLTAVKVTWNGNLSISNKGWDLILPOASNNNGNYRCIGYGDENDVFRLN 180
QY 180 TVKIQVQEPPTREPVLRASSFPQISGNPVTILTCETQLSLERSDVPLFRFRFRDDOTLGLCW 239
Db 181 FKIIKIQLFPPHKLKATDSQPTGEGSVNLSCETQLPERSDTPLFHNFRRGEVILSDW 240
QY 240 SLSNPNQITAMWSKDSGFWCKAATMPHVSVIDSPRSWIQVQ-IPASHPVLTLSPEKALN 298
Db 241 STYPELQLFTVWRENSGSYWCAGAEIVRGNIHKHPSLQIHVQIPVSGVLLLETQPSGGQA 300
QY 299 FEETKVTLCETQEDSLRLTYRPHYEGV--PLRHKSVCRCERGASISFSLTTENSNGNYCT 356
Db 301 VEGEMLVVCSVNAEGTDTTFSHREDMQESLGRKTQSLRAELELPAIRQSHAGGYCT 360
QY 357 ADNLGAKPSKAVSLSTVPSVHPVNLSSPEDLIPEGA-----KVTLHCEAQ 404
Db 361 ADNSYG--PVQSMVLNVTVRETP-----GNRDLVAAGATGGLSALLAVALLFHCWR 413
QY 405 RGS 407
Db 414 RKS 416

RESULT 13
Q8N732 PRELIMINARY; PRT; 360 AA.
AC Q8N732;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DJ801G22.1 (Novel immunoglobulin domain protein similar to
DE immunoglobulin receptors) (Fragment).
GN Name=DJ801G22.1;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bagguley C.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL135929; CAB92753.1; -.
DR HSSP; P12319; 1F2Q.
DR GO; GO:0004872; P:receptor activity; IEA.
DR InterPro; IPR007110; I9-like.
DR InterPro; IPR003598; I9_C2.
DR Pfam; PF00047; I9; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
KW Receptor.
FT NON_TER 1
FT NON_TER 360 360
SQ SEQUENCE 360 AA.; 40724 MW; 7ACC2E7FA3256D62 CRC64;

Query Match 19.3%; Score 772; DB 2; Length 360;
Best Local Similarity 46.1%; Pred. No. 1.2e-43;
Matches 165; Conservative 49; Mismatches 138; Indels 6; Gaps 4;

QY 22 RPIILQBPWTVFQGEVTLTKGFRYSQKWKWHYLGKELLRTPTDNLVEQSG 81
Db 4 KPVLSVHPPTWTFKGERVILTCNGQFYATEKTTWYHVGKELTTPGNTLEVRSG 63
QY 82 EYRCQAQSGPLSPVHLDPSSASLILQAPLSVFEQDSVVLRCRAKAEVTLNNTIYK-NDN 140
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Db 64 LYRCQAQSGPRSPVRLFFSSDSLILQAPYSVFEQDTLVLRCHRRKEKLTAVKVTWNGN 123
QY 141 VLAFLNKRDTDFHPIHACLDKNGAYRCTGYKESCCPVSNNTVKIQVQEPPTREPVLRASSFO 200
Db 124 ILSISNKSWDLLIPQASNNNGNYRCIGYGDENDVFRSNFKIIKIQLFPPHKLKATDSQ 183
QY 201 PISGNPVTILTCETQLSLERSDVPLFRFRFRDDOTLGLGWSLSPNPQITAMWSKDSGFWYC 260
Db 184 PTEGNSVNLSCETQLPERSDTPLFHNFRRGEVILSDWSTYPELQLFTVWRENSGSYWC 243
QY 261 KAATMPHVSVIDSPRSWIQVQ-IPASHPVLTLSPEKALNFEETKVTLCETQEDSLRLTY 319
Db 244 GAETVRGNIHKHPSLQIHVQIPVSGVLLLETQPSGGQAVEGEMLVVCSVNAEGTDTTF 303
QY 320 RPYHEGV--PLRHKSVCRCERGASISFSLTTENSNGNYCTADNGLGAKPSKAVSLSTV 375
Db 304 SWHREDMQESLGRKTQSLRAELELPAIRQSHAGGYCTADNSYG--PVQSMVLNVTV 359

RESULT 14
Q8BJA5 PRELIMINARY; PRT; 508 AA.
AC Q8BJA5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus activated spleen cDNA, RIKEN full-length enriched
DE library, clone:FB30015F10 product:weakly similar to SH2 DOMAIN-
DE CONTAINING PHOSPHATASE ANCHOR PROTEIN 1C.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Activated spleen;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
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RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RN Genome Res. 10:1757-1771(2000).
RN [6]
RC SEQUENCE FROM N.A.
RP STRAIN=NOD; TISSUE=Activated spleen;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hitaoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Komoto H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohashi N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR HSSP; AK089756; BAC40954.1;
DR HSSP; P12319; IP2Q.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
SQ SEQUENCE 508 AA; 56795 MW; 2777AA4733A9443F CRC64;

Query Match 17.3%; Score 692.5; DB 2; Length 508;
Best Local Similarity 40.9%; Pred. No. 4.1e-38;
Matches 160; Conservative 63; Mismatches 131; Indels 37; Gaps 6;

QY 105 LILQAPLSVPEGSVLRCAKAEVTLN-TIYKNDNLVLAFLNKRDTDFHPLACLKNGA 163
DB 31 LVLPAPVAVPEGSVLRCAKAEVTLN-TIYKNDNLVLAFLNKRDTDFHPLACLKNGQ 90

QY 164 YRCTGYKESC--CPVSNNTVKIQVPPFTPLVLRASSFPQISGNVTLTCTQLSLERSD 221
DB 91 YKCTSKKWKSGSLYTSNTVRVQVQLFPPRPLRPSHPIDGSPVTLTCTQLSAKSD 150

QY 222 VPLRFRFRDQTLGLGWSLSPNFOITAMWSKDSGFYWCXAAWPHSVISDSRPSVIOV 281
DB 151 ARLOQCFRRLLQLGSGCRSSBFHPAIWTEESKRYQCKAETVNSQVRKQSTAFIPVQ 210

QY 282 IPASHPVLTLSPEKALNFECTKVTLCETQEDSLRTLRYFYHEGVP-----LRH 330
DB 211 RASARFQTHIIIPASKLVFEGQLLLNCSV-----KGVFQPLKFSYWKDMLN 257

QY 331 KSVRCBERGASISFLATTEN---SGNYCTADNGLGAKPSKAVSLSVTVPSHPVLMNLSSP 387
DB 258 KETKILKSSNAEPKISQVNSIDAGEYHREATNSRRSFVSRAFTITIKVPVSPVLTSTG 317

QY 388 EDLIFPGAKVTLHCEAQRGLPILYQFHEDDALEARRSANGAGVAISPLTAHESGNY 447
DB 318 KTOALEGDLMTLHCQSQRGSPCLIFEFYFVNSLGNSSILSGGAYNFMSRSGNY 377

QY 448 CTADNCGFGPORSKAVLSL-----TVPVVS 471
DB 378 CTADNGLGACQSAIRISIFDMTKNSVPWA 408

RESULT 15
QY1VK7 PRELIMINARY; PRT; 509 AA.
AC QY1VK7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Macrophage scavenger receptor 2 (Fc receptor-like protein 2 scavenger isoform).
GN Name=Msr2; Synonyms=FcRh2;
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=15302849;
RA Davis R.S., Stephan R.P., Chen C.C., Dennis G. Jr., Cooper M.D.;
RT "Differential B cell expression of mouse Fc receptor homologs.";
RL Int. Immunol. 16:1343-1353(2004).
DR EMBL; BC016551; AAH16551.1; -;
DR EMBL; AY508556; AAS91576.1; -;
DR HSSP; Q08380; IBY2.
DR MGD; MGI:1933397; Msr2.
DR GO; GO:0005615; C:extracellular space; TAS.
DR Pfam; PF00047; ig; 3.
DR PRINTS; PR00530; SRCR; 1.
DR SMART; SM00258; SPERACTRCPTR.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00420; SRCR; 1.
DR PROSITE; PS0287; SRCR_2; 1.
KW Receptor.
SQ SEQUENCE 509 AA; 55757 MW; 25989021E6AF772B CRC64;

Query Match 16.2%; Score 647; DB 2; Length 509;
Best Local Similarity 28.0%; Pred. No. 4.6e-35;
Matches 166; Conservative 69; Mismatches 157; Indels 200; Gaps 11;

QY 96 VHLDFSSASLILQAPLSVPEGSVLRCAKAEVTLNNTIYKNDNV-LAFLNKRDTDFHIP 154
DB 15 VQSDMLSL---PHRSYEGDQVVISCTGKNGDIKRLKYKDGVIHYIYSSASVYTR 70

QY 155 HACLKNDGAYRCYGYKESCPV-----SSNTVKIQVEPFTPLVLRASSFPISGNVTLT 210
DB 71 NARRGDSGYSCKADKRFLLFIDTTEETGSKMLNVOELFPAPGLTASLPQVEGSSVTL 130

QY 211 CETQLSLERSDVLPRFRFRDQTLGLGWSLSPNFOITAMWSKDSGFYWCXAAWPHSVI 270
DB 131 CNTWLPSDRATQLRYSFFKDGHTLQSGWT-SSKFTTSAISKDSGNYCEANTASRSVS 189

QY 271 SDSPRSWIOVQ-IPASHPVLTLSPEKALNFECTKVTLCETQEDSLRTLRYFYHEGVPLR 329

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Db      190 KQSHRSYIDVERIPVSQVTMEIQPSRGWVEG----- 221
QY      330 HKSVRCERGASISFSLTTENSGNYCYCTADNGLCAKPSKAVSLVTVVSHPVNLNLSSPED 389
Db      222 -----EP 223
QY      390 LIFEKAVTLHCEAQRGSLPILYQFHEDAALERRRANGSAGGVAISFSLTAHSGNYCYCT 449
Db      224 LVVEGEPLVLACSVAKGTGLITFSHRQD-----TKESVGK----- 259
QY      450 ADNGFGPQSKAVSLITVPVSHPVLTLSAEALTPEGATVTLHCEVQRGSPQILYQFYH 509
Db      260 -----KSQRSQVELEIP----- 272
QY      510 EDMPLWSSSTPSVGRVSFSLTEGHSNGNYCYCTADNGFGPQRSEVVSFVTVVPSRPILT 569
Db      273 -----TIREGHAGGYCTADNNYGLIOSAIVNITVKIPVNLPLLS 312
QY      570 LRVPRQAQVVGDLLELHCEAPRGSPILYWFYHEDVTLGSSAPSGGEASFNLSTAEHS 629
Db      313 ISVPGVLPFIDGVAELHCEDKRASPPVLYWFYHENITLANTSAFPGKASFKLSTAGHS 372
QY      630 GNYSCAANGLVAQHSOTISLVIVVPSRPILTFRAPRAQVVGDLLELHCE 681
Db      373 GNYSCAENAWGTRSEVTVLNVTEP-----PPKVRLVNG---PHHCE 412

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